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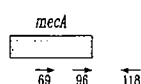
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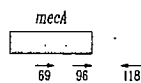
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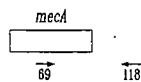
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(54) Title: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT *STAPHYLOCCOCUS AUREUS*

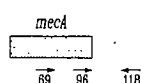
MREJ Type iv



MREJ Type v

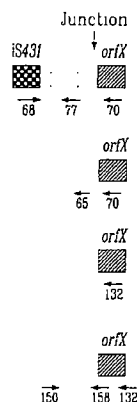


MREJ Type vi

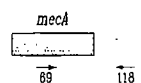


MREJ Type vii

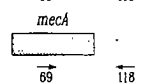
← or → Primer

(57) Abstract: The present invention describes novel SCCmec right extremity junction sequences for the detection of methicillin-resistant *Staphylococcus aureus* (MRSA). It relates to the use of these DNA sequences for diagnostic purposes.

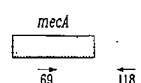
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MREJ Type viii

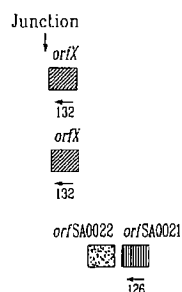


MREJ Type ix



MREJ Type x

← or → Primer



B

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SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT *STAPHYLOCOCCUS AUREUS*

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BACKGROUND OF THE INVENTION

Clinical significance of *Staphylococcus aureus*

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The coagulase-positive species *Staphylococcus aureus* is well documented as a human opportunistic pathogen. Nosocomial infections caused by *S. aureus* are a major cause of morbidity and mortality. Some of the most common infections caused by *S. aureus* involve the skin, and they include furuncles or boils, cellulitis, impetigo, and postoperative wound infections at various sites. Some of the more serious infections produced by *S. aureus* are bacteremia, pneumonia, osteomyelitis, acute endocarditis, myocarditis, pericarditis, cerebritis, meningitis, scalded skin syndrome, and various abscesses. Food poisoning mediated by staphylococcal enterotoxins is another important syndrome associated with *S. aureus*. Toxic shock syndrome, a community-acquired disease, has also been attributed to infection or colonization with toxigenic *S. aureus* (Murray *et al.* Eds, 1999, Manual of Clinical Microbiology, 7th Ed., ASM Press, Washington, D.C.).

20

Methicillin-resistant *S. aureus* (MRSA) emerged in the 1980s as a major clinical and epidemiologic problem in hospitals. MRSA are resistant to all β -lactams including penicillins, cephalosporins, carbapenems, and monobactams, which are the most commonly used antibiotics to cure *S. aureus* infections. MRSA infections can only be treated with more toxic and more costly antibiotics, which are normally used as the last line of defence. Since MRSA can spread easily from patient to patient via personnel, hospitals over the world are confronted with the

30

problem to control MRSA. Consequently, there is a need to develop rapid and simple screening or diagnostic tests for detection and/or identification of MRSA to reduce its dissemination and improve the diagnosis and treatment of infected patients.

5

Methicillin resistance in *S. aureus* is unique in that it is due to acquisition of DNA from other coagulase-negative staphylococci (CNS), coding for a supernumerary β -lactam-resistant penicillin-binding protein (PBP), which takes over the biosynthetic functions of the normal PBPs when the cell is exposed to β -lactam antibiotics. *S. aureus* normally contains four PBPs, of which PBPs 1, 2 and 3 are essential. The low-affinity PBP in MRSA, termed PBP 2a (or PBP2'), is encoded by the chromosomal *mecA* gene and functions as a β -lactam-resistant transpeptidase. The *mecA* gene is absent from methicillin-sensitive *S. aureus* but is widely distributed among other species of staphylococci and is highly conserved
15 (Ubukata *et al.*, 1990, Antimicrob. Agents Chemother. **34**:170-172).

By nucleotide sequence determination of the DNA region surrounding the *mecA* gene from *S. aureus* strain N315 (isolated in Japan in 1982), Hiramatsu *et al.* have found that the *mecA* gene is carried by a novel genetic element, designated
20 staphylococcal cassette chromosome *mec* (SCC*mec*), inserted into the chromosome. SCC*mec* is a mobile genetic element characterized by the presence of terminal inverted and direct repeats, a set of site-specific recombinase genes (*ccrA* and *ccrB*), and the *mecA* gene complex (Ito *et al.*, 1999, Antimicrob. Agents Chemother. **43**:1449-1458; Katayama *et al.*, 2000, Antimicrob. Agents Chemother.
25 **44**:1549-1555). The element is precisely excised from the chromosome of *S. aureus* strain N315 and integrates into a specific *S. aureus* chromosomal site in the same orientation through the function of a unique set of recombinase genes comprising *ccrA* and *ccrB*. Two novel genetic elements that shared similar structural features of SCC*mec* were found by cloning and sequencing the DNA

region surrounding the *mecA* gene from MRSA strains NCTC 10442 (the first MRSA strain isolated in England in 1961) and 85/2082 (a strain from New Zealand isolated in 1985). The three SCC*mec* have been designated type I (NCTC 10442), type II (N315) and type III (85/2082) based on the year of isolation of the strains (Ito *et al.*, 2001, Antimicrob. Agents Chemother. **45**:1323-1336) (Figure 1). Hiramatsu *et al.* have found that the SCC*mec* DNAs are integrated at a specific site in the methicillin-sensitive *S. aureus* (MSSA) chromosome. They characterized the nucleotide sequences of the regions around the left and right boundaries of SCC*mec* DNA (i.e. *attL* and *attR*, respectively) as well as those of the regions around the SCC*mec* DNA integration site (i.e. *attB_{scc}* which is the bacterial chromosome attachment site for SCC*mec* DNA). The *attB_{scc}* site was located at the 3' end of a novel open reading frame (ORF), *orfX*. The *orfX* potentially encodes a 159-amino acid polypeptide sharing identity with some previously identified polypeptides, but of unknown function (Ito *et al.*, 1999, Antimicrob. Agents Chemother. **43**:1449-1458). Recently, a new type of SCC*mec* (type IV) has been described by both Hiramatsu *et al.* (Ma *et al.*, 2002, Antimicrob. Agents Chemother. **46**:1147-1152) and Oliveira *et al.* (Oliveira *et al.*, 2001, Microb. Drug Resist. **7**:349-360). The sequences of the right extremity of the new type IV SCC*mec* from *S. aureus* strains CA05 and 8/6-3P published by Hiramatsu *et al.* (Ma *et al.*, 2002, Antimicrob. Agents Chemother. **46**:1147-1152) were nearly identical over 2000 nucleotides to that of type II SCC*mec* of *S. aureus* strain N315 (Ito *et al.*, 2001, Antimicrob. Agents Chemother. **45**:1323-1336). No sequence at the right extremity of the SCC*mec* type IV is available from the *S. aureus* strains HDE288 and PL72 described by Oliveira *et al.* (Oliveira *et al.*, 2001, Microb. Drug Resist. **7**:349-360).

Previous methods used to detect and identify MRSA (Saito *et al.*, 1995, J. Clin. Microbiol. **33**:2498-2500; Ubukata *et al.*, 1992, J. Clin. Microbiol. **30**:1728-1733; Murakami *et al.*, 1991, J. Clin. Microbiol. **29**:2240-2244; Hiramatsu *et al.*, 1992,

Microbiol. Immunol. **36**:445-453), which are based on the detection of the *mecA* gene and *S. aureus*-specific chromosomal sequences, encountered difficulty in discriminating MRSA from methicillin-resistant coagulase-negative staphylococci (CNS) because the *mecA* gene is widely distributed in both *S. aureus* and CNS species (Suzuki *et al.*, 1992, Antimicrob. Agents. Chemother. **36**:429-434). Hiramatsu *et al.* (US patent 6,156,507) have described a PCR assay specific for MRSA by using primers that can specifically hybridize to the right extremities of the 3 types of SCC*mec* DNAs in combination with a primer specific to the *S. aureus* chromosome, which corresponds to the nucleotide sequence on the right side of the SCC*mec* integration site. Since nucleotide sequences surrounding the SCC*mec* integration site in other staphylococcal species (such as *S. epidermidis* and *S. haemolyticus*) are different from those found in *S. aureus*, this PCR assay was specific for the detection of MRSA. This PCR assay also supplied information for MREP typing (standing for «*mec* right extremity polymorphism») of SCC*mec* DNA (Ito *et al.*, 2001, Antimicrob. Agents Chemother. **45**:1323-1336; Hiramatsu *et al.*, 1996, J. Infect. Chemother. **2**:117-129). This typing method takes advantage of the polymorphism at the right extremity of SCC*mec* DNAs adjacent to the integration site among the three types of SCC*mec*. Type III has a unique nucleotide sequence while type II has an insertion of 102 nucleotides to the right terminus of SCC*mec* type I. The MREP typing method described by Hiramatsu *et al.* (Ito *et al.*, 2001, Antimicrob. Agents Chemother. **45**:1323-1336; Hiramatsu *et al.*, 1996, J. Infect. Chemother. **2**:117-129) defines the SCC*mec* type I as MREP type i, SCC*mec* type II as MREP type ii and SCC*mec* type III as MREP type iii. It should be noted that the MREP typing method cannot differentiate the new SCC*mec* type IV described by Hiramatsu *et al.* (Ma *et al.*, 2002, Antimicrob. Agents Chemother. **46**:1147-1152) from SCC*mec* type II because these two SCC*mec* types exhibit the same nucleotide sequence to the right extremity.

The set of primers described by Hiramatsu et al. as being the optimal primer combination (SEQ ID NOs.: 22, 24, 28 in US patent 6,156,507 corresponding to SEQ ID NOs.: 56, 58 and 60, respectively, in the present invention) have been used in the present invention to test by PCR a variety of MRSA and MSSA strains (Figure 1 and Table 1). Twenty of the 39 MRSA strains tested were not amplified by the Hiramatsu et al. multiplex PCR assay (Tables 2 and 3). Hiramatsu's method indeed was successful in detecting less than 50% of the tested 39 MRSA strains. This finding demonstrates that some MRSA strains have sequences at the right extremity of SCCmec-chromosome right extremity junction different from those identified by Hiramatsu *et al.* Consequently, the system developed by Hiramatsu *et al.* does not allow the detection of all MRSA. The present invention relates to the generation of SCCmec-chromosome right extremity junction sequence data required to detect more MRSA strains in order to improve the Hiramatsu *et al.* assay. There is a need for developing more ubiquitous primers and probes for the detection of most MRSA strains around the world.

SUMMARY OF THE INVENTION

It is an object of the present invention to provide a specific, ubiquitous and sensitive method using probes and/or amplification primers for determining the presence and/or amount of nucleic acids from all MRSA strains.

Ubiquity of at least 50% amongst the strains representing MRSA strains types IV to X is an objective of this invention.

Therefore, in accordance with the present invention is provided a method to detect the presence of a methicillin-resistant *Staphylococcus aureus* (MRSA) strain in a sample, the MRSA strain being resistant because of the presence of an SCCmec

insert containing a *mecA* gene, said *SCCmec* being inserted in bacterial nucleic acids thereby generating a polymorphic right extremity junction (MREJ), the method comprising the step of annealing the nucleic acids of the sample with a plurality of probes and/or primers, characterized by:

- 5 (i) the primers and/or probes are specific for MRSA strains and capable of annealing with polymorphic MREJ nucleic acids, the polymorphic MREJ comprising MREJ types i to x; and
 - (ii) the primers and/or probes altogether can anneal with at least four MREJ types selected from MREJ types i to x.
- 10 In a specific embodiment, the primers and/or probes are all chosen to anneal under common annealing conditions, and even more specifically, they are placed altogether in the same physical enclosure.

A specific method has been developed using primers and/or probes having at least 10 nucleotides in length and capable of annealing with MREJ types i to iii, defined
 15 in any one of SEQ ID NOs: 1, 20, 21, 22, 23, 24, 25, 41, 199 ; 2, 17, 18, 19, 26, 40, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 185, 186, 197 ; 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 104, 184, 198 and with one or more of MREJ types iv to ix, having SEQ ID NOs: 42, 43, 44, 45, 46, 51 ; 47, 48, 49, 50 ; 171 ; 165, 166 ; 167 ; 168. To be perfectly ubiquitous with the all the sequenced MREJs, the
 20 primers and/or probes altogether can anneal with said SEQ ID NOs of MREJ types i to ix.

The following specific primers and/or probes having the following sequences have been designed:

25 66, 100, 101, 105, 52, 53, 54, 55, 56, 57, 64, 71, 72, 73, 74, 75, 76, 70, 103, 130, 132, 158, 159, 59, 62, 126, 127, 128, 129, 131, 200, 201, 60, 61, 63 32, 83, 84, 160, 161, 162, 163, 164 30 85, 86, 87, 88, 89	for the detection of MREJ type i
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66, 97, 99, 100, 101, 106, 117, for the detection of MREJ type ii
 118, 124, 125, 52, 53, 54, 55, 56, 57
 64, 71, 72, 73, 74, 75, 76, 70,
 103, 130, 132, 158, 159
 5 59, 62
 126, 127
 128, 129, 131, 200, 201
 60, 61, 63
 32, 83, 84, 160, 161, 162, 163, 164
 10 85, 86, 87, 88, 89

67, 98, 102, 107, 108 for the detection of MREJ type iii
 64, 71, 72, 73, 74, 75, 76, 70,
 103, 130, 132, 158, 159
 15 58,
 59, 62
 126, 127
 128, 129, 131, 200, 201
 60, 61, 63
 20 32, 83, 84, 160, 161, 162, 163, 164
 85, 86, 87, 88, 89

79, 77, 145, 147 for the detection of MREJ type iv
 64, 71, 72, 73, 74, 75, 76, 70,
 25 103, 130, 132, 158, 159
 59, 62
 126, 127
 128, 129, 131, 200, 201
 60, 61, 63
 30 68
 32, 83, 84, 160, 161, 162, 163, 164
 85, 86, 87, 88, 89

65, 80, 146, 154, 155 for the detection of MREJ type v
 35 64, 71, 72, 73, 74, 75, 76,
 70, 103, 130, 132, 158, 159
 59, 62
 126, 127
 128, 129, 131, 200, 201
 40 60, 61, 63
 32, 83, 84, 160, 161, 162, 163, 164
 85, 86, 87, 88, 89

202, 203, 204

for the detection of MREJ type vi

64, 71, 72, 73, 74, 75, 76, 70,

103, 130, 132, 158, 159

59, 62

5 126, 127

128, 129, 131, 200, 201

60, 61, 63

32, 83, 84, 160, 161, 162, 163, 164

85, 86, 87, 88, 89

10

112, 113, 114, 119, 120, 121, 122

for the detection of MREJ type vii,

123, 150, 151, 153

64, 71, 72, 73, 74, 75, 76, 70, 103,

130, 132, 158, 159

15 59, 62

126, 127

128, 129, 131, 200, 201

60, 61, 63

32, 83, 84, 160, 161, 162, 163, 164

20 85, 86, 87, 88, 89

115, 116, 187, 188, 207, 208 for the detection of MREJ type viii

64, 71, 72, 73, 74, 75, 76, 70,

103, 130, 132, 158, 159

25 59, 62

126, 127

128, 129, 131, 200, 201

60, 61, 63

32, 83, 84, 160, 161, 162, 163, 164

30 85, 86, 87, 88, 89

109, 148, 149, 205, 206

for the detection of MREJ type ix.

64, 71, 72, 73, 74, 75, 76

70, 103, 130, 132, 158, 159

35 59, 62

126, 127

128, 129, 131, 200, 201

60, 61, 63

32, 83, 84, 160, 161, 162, 163, 164

40 85, 86, 87, 88, 89

Amongst these, the following primer pairs having the following sequences are used:

- | | | |
|----|-------------------------------------|-------------------------------------|
| | 64/66, 64/100, 64/101; 59/52, | for the detection of type i MREJ |
| | 59/53, 59/54, 59/55, 59/56, 59/57, | |
| 5 | 60/52, 60/53, 60/54, 60/55, 60/56 | |
| | 60/57, 61/52, 61/53, 61/54, 61/55 | |
| | 61/56, 61/57, 62/52, 62/53, 62/54 | |
| | 62/55, 62/56, 62/57, 63/52, 63/53 | |
| | 63/54, 63/55, 63/56, 63/57 | |
| 10 | | |
| | 64/66, 64/97, 64/99, 64/100, 64/101 | for the detection of type ii MREJ |
| | 59/52, 59/53, 59/54, 59/55, 59/56, | |
| | 59/57, 60/52, 60/53, 60/54, 60/55, | |
| | 60/56, 60/57, 61/52, 61/53, 61/54, | |
| 15 | 61/55, 61/56, 61/57, 62/52, 62/53, | |
| | 62/54, 62/55, 62/56, 62/57, 63/52 | |
| | 63/53, 63/54, 63/55, 63/56, 63/57 | |
| | | |
| | 64/67, 64/98, 64/102 ; 59/58, | for the detection of type iii MREJ |
| 20 | 60/58, 61/58, 62/58, 63/58 | |
| | | |
| | 64/79 | for the detection of type iv MREJ |
| | 64/80 | for the detection of type v MREJ |
| | 64/204 | for the detection of type vi MREJ |
| 25 | 64/112, 64/113 | for the detection of type vii MREJ |
| | 64/115, 64/116 | for the detection of type viii MREJ |
| | 64/109 | for the detection of type ix MREJ |

As well, amongst these, the following probes having the following sequences are used:

SEQ ID NOs: 32, 83, 84, 160, 161, 162, 163, 164 for the detection of MREJ types i to ix.

In the most preferred embodied method, the following primers and/or probes having the following nucleotide sequences are used together. The preferred combinations make use of:

- 5 i) SEQ ID NOs: 64, 66, 84, 163, 164 for the detection of MREJ type i
- ii) SEQ ID NOs: 64, 66, 84, 163, 164 for the detection of MREJ type ii
- iii) SEQ ID NOs: 64, 67, 84, 163, 164 for the detection of MREJ type iii
- iv) SEQ ID NOs: 64, 79, 84, 163, 164 for the detection of MREJ type iv
- v) SEQ ID NOs: 64, 80, 84, 163, 164 for the detection of MREJ type v
- 10 vi) SEQ ID NOs: 64, 112, 84, 163, 164 for the detection of MREJ type
- vii.

All these probes and primers can even be used together in the same physical enclosure.

- 15 It is another object of this invention to provide a method for typing a MREJ of a MRSA strain, which comprises the steps of: reproducing the above method with primers and/or probes specific for a determined MREJ type, and detecting an annealed probe or primer as an indication of the presence of a determined MREJ type.
- 20 It is further another object of this invention to provide a nucleic acid selected from SEQ ID NOs:
 - i) SEQ ID NOs: 42, 43, 44, 45, 46, 51 for sequence of MREJ type iv ;
 - ii) SEQ ID NOs: 47, 48, 49, 50 for sequence of MREJ type v ;
 - iii) SEQ ID NOs: 171 for sequence of MREJ type vi ;
 - 25 iv) SEQ ID NOs: 165, 166 for sequence of MREJ type vii ;
 - v) SEQ ID NOs: 167 for sequence of MREJ type viii ;
 - vi) SEQ ID NOs: 168 for sequence of MREJ type ix.

Oligonucleotides of at least 10 nucleotides in length which hybridize with any of these nucleic acids and which hybridize with one or more MREJ of types selected from iv to ix are also objects of this invention. Amongst these, primer pairs (or probes) having the following SEQ ID NOs:

- 5 64/66, 64/100, 64/101; 59/52, for the detection of type i MREJ
 59/53, 59/54, 59/55, 59/56, 59/57,
 60/52, 60/53, 60/54, 60/55, 60/56
 60/57, 61/52, 61/53, 61/54, 61/55
 61/56, 61/57, 62/52, 62/53, 62/54
 10 62/55, 62/56, 62/57, 63/52, 63/53
 63/54, 63/55, 63/56, 63/57
- 64/66, 64/97, 64/99, 64/100, 64/101 for the detection of type ii MREJ
 59/52, 59/53, 59/54, 59/55, 59/56,
 15 59/57, 60/52, 60/53, 60/54, 60/55,
 60/56, 60/57, 61/52, 61/53, 61/54,
 61/55, 61/56, 61/57, 62/52, 62/53,
 62/54, 62/55, 62/56, 62/57, 63/52
 63/53, 63/54, 63/55, 63/56, 63/57
 20
- 64/67, 64/98, 64/102 ; 59/58, for the detection of type iii MREJ
 60/58, 61/58, 62/58, 63/58
- 64/79 for the detection of type iv MREJ
 25 64/80 for the detection of type v MREJ
 64/204 for the detection of type vi MREJ
 64/112, 64/113 for the detection of type vii MREJ
 64/115, 64/116 for the detection of type viii MREJ
 64/109 for the detection of type ix MREJ,
 30 are also within the scope of this invention.

Further, internal probes having nucleotide sequences defined in any one of SEQ ID NOs: 32, 83, 84, 160, 161, 162, 163, 164, are also within the scope of this invention. Compositions of matter comprising the primers and/or probes annealing or hybridizing with one or more MREJ of types selected from iv to ix as well as with
 5 the above nucleic acids, comprising or not primers and/or probes, which hybridize with one or more MREJ of types selected from i to iii, are further objects of this invention. The preferred compositions would comprise the primers having the nucleotide sequences defined in SEQ ID NOs:

64/66, 64/100, 64/101; 59/52, for the detection of type i MREJ

10 59/53, 59/54, 59/55, 59/56, 59/57,
 60/52, 60/53, 60/54, 60/55, 60/56
 60/57, 61/52, 61/53, 61/54, 61/55
 61/56, 61/57, 62/52, 62/53, 62/54
 62/55, 62/56, 62/57, 63/52, 63/53
 15 63/54, 63/55, 63/56, 63/57

64/66, 64/97, 64/99, 64/100, 64/101 for the detection of type ii MREJ
 59/52, 59/53, 59/54, 59/55, 59/56,
 59/57, 60/52, 60/53, 60/54, 60/55,
 20 60/56, 60/57, 61/52, 61/53, 61/54,
 61/55, 61/56, 61/57, 62/52, 62/53,
 62/54, 62/55, 62/56, 62/57, 63/52
 63/53, 63/54, 63/55, 63/56, 63/57

25 64/67, 64/98, 64/102 ; 59/58, for the detection of type iii MREJ
 60/58, 61/58, 62/58, 63/58

64/79 for the detection of type iv MREJ

64/80 for the detection of type v MREJ

30 64/204 for the detection of type vi MREJ

64/112, 64/113 for the detection of type vii MREJ

64/115, 64/116 for the detection of type viii MREJ

64/109 for the detection of type ix MREJ,

or probes, which SEQ ID NOs are: 32, 83, 84, 160, 161, 162, 163, 164, or both.

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DETAILED DESCRIPTION OF THE INVENTION

Here is particularly provided a method wherein each of MRSA nucleic acids or a variant or part thereof comprises a selected target region hybridizable with said primers or probes developed to be ubiquitous;

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wherein each of said nucleic acids or a variant or part thereof comprises a selected target region hybridizable with said primers or probes ;

said method comprising the steps of contacting said sample with said probes or primers and detecting the presence and/or amount of hybridized probes or amplified products as an indication of the presence and/or amount of MRSA.

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In the method, sequences from DNA fragments of SCC*mec*-chromosome right extremity junction, thereafter named MREJ standing for « *mec* right extremity junction » including sequences from SCC*mec* right extremity and chromosomal DNA to the right of the SCC*mec* integration site are used as parental sequences from which are derived the primers and/or the probes. MREJ sequences include our proprietary sequences as well as sequences obtained from public databases and from US patent 6,156,507 and were selected for their capacity to sensitively, specifically, ubiquitously and rapidly detect the targeted MRSA nucleic acids.

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Our proprietary DNA fragments and oligonucleotides (primers and probes) are also another object of this invention.

Composition of matters such as diagnostic kits comprising amplification primers or probes for the detection of MRSA are also objects of the present invention.

In the above methods and kits, probes and primers are not limited to nucleic acids and may include, but are not restricted to, analogs of nucleotides. The diagnostic reagents constituted by the probes and the primers may be present in any suitable
5 form (bound to a solid support, liquid, lyophilized, etc.).

In the above methods and kits, amplification reactions may include but are not restricted to: a) polymerase chain reaction (PCR), b) ligase chain reaction (LCR), c) nucleic acid sequence-based amplification (NASBA), d) self-sustained sequence
10 replication (3SR), e) strand displacement amplification (SDA), f) branched DNA signal amplification (bDNA), g) transcription-mediated amplification (TMA), h) cycling probe technology (CPT), i) nested PCR, j) multiplex PCR, k) solid phase amplification (SPA), l) nuclease dependent signal amplification (NDSA), m) rolling circle amplification technology (RCA), n) Anchored strand displacement
15 amplification, o) Solid-phase (immobilized) rolling circle amplification.

In the above methods and kits, detection of the nucleic acids of target genes may include real-time or post-amplification technologies. These detection technologies can include, but are not limited to fluorescence resonance energy transfer (FRET)-
20 based methods such as adjacent hybridization of probes (including probe-probe and probe-primer methods), *TaqMan* probe, molecular beacon probe, Scorpion probe, nanoparticle probe and Amplifluor probe. Other detection methods include target gene nucleic acids detection via immunological methods, solid phase hybridization methods on filters, chips or any other solid support. In these systems,
25 the hybridization can be monitored by fluorescence, chemiluminescence, potentiometry, mass spectrometry, plasmon resonance, polarimetry, colorimetry, flow cytometry or scanometry. Nucleotide sequencing, including sequencing by dideoxy termination or sequencing by hybridization (e.g. sequencing using a DNA

chip) represents another method to detect and characterize the nucleic acids of target genes.

In a preferred embodiment, a PCR protocol is used for nucleic acid amplification.

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A method for detection of a plurality of potential MRSA strains having different MREJ types may be conducted in separate reactions and physical enclosures, one type at the time. Alternatively, it could be conducted simultaneously for different types in separate physical enclosures, or in the same physical enclosures. In the latter scenario a multiplex PCR reaction could be conducted which would require that the oligonucleotides are all capable of annealing with a target region under common conditions. Since many probes or primers are specific for a determined MREJ type, typing a MRSA strain is a possible embodiment. When a mixture of oligonucleotides annealing together with more than one type is used in a single physical enclosure or container, different labels would be used to distinguish one type from another.

We aim at developing a DNA-based test or kit to detect and identify MRSA. Although the sequences from *orfX* genes and some *SCCmec* DNA fragments are available from public databases and have been used to develop DNA-based tests for detection of MRSA, new sequence data allowing to improve MRSA detection and identification which are object of the present invention have either never been characterized previously or were known but not shown to be located at the right extremity of *SCCmec* adjacent to the integration site (Table 4). These novel sequences could not have been predicted nor detected by the MRSA-specific PCR assay developed by Hiramatsu *et al.* (US patent 6,156,507). These sequences will allow to improve current DNA-based tests for the diagnosis of MRSA because they allow the design of ubiquitous primers and probes for the detection and

identification of more MRSA strains including all the major epidemic clones from around the world.

The diagnostic kits, primers and probes mentioned above can be used to detect and/or identify MRSA, whether said diagnostic kits, primers and probes are used for *in vitro* or *in situ* applications. The said samples may include but are not limited to: any clinical sample, any environmental sample, any microbial culture, any microbial colony, any tissue, and any cell line.

It is also an object of the present invention that said diagnostic kits, primers and probes can be used alone or in combination with any other assay suitable to detect and/or identify microorganisms, including but not limited to: any assay based on nucleic acids detection, any immunoassay, any enzymatic assay, any biochemical assay, any lysotypic assay, any serological assay, any differential culture medium, any enrichment culture medium, any selective culture medium, any specific assay medium, any identification culture medium, any enumeration culture medium, any cellular stain, any culture on specific cell lines, and any infectivity assay on animals.

In the methods and kits described herein below, the oligonucleotide probes and amplification primers have been derived from larger sequences (i.e. DNA fragments of at least 100 base pairs). All DNA sequences have been obtained either from our proprietary sequences or from public databases (Tables 5, 6, 7, 8 and 9).

It is clear to the individual skilled in the art that oligonucleotide sequences other than those described in the present invention and which are appropriate for detection and/or identification of MRSA may also be derived from the proprietary fragment sequences or selected public database sequences. For example, the

oligonucleotide primers or probes may be shorter but of a length of at least 10 nucleotides or longer than the ones chosen; they may also be selected anywhere else in the proprietary DNA fragments or in the sequences selected from public databases; they may also be variants of the same oligonucleotide. If the target DNA or a variant thereof hybridizes to a given oligonucleotide, or if the target DNA or a variant thereof can be amplified by a given oligonucleotide PCR primer pair, the converse is also true; a given target DNA may hybridize to a variant oligonucleotide probe or be amplified by a variant oligonucleotide PCR primer. Alternatively, the oligonucleotides may be designed from said DNA fragment sequences for use in amplification methods other than PCR. Consequently, the core of this invention is the detection and/or identification of MRSA by targeting genomic DNA sequences which are used as a source of specific and ubiquitous oligonucleotide probes and/or amplification primers. Although the selection and evaluation of oligonucleotides suitable for diagnostic purposes require much effort, it is quite possible for the individual skilled in the art to derive, from the selected DNA fragments, oligonucleotides other than the ones listed in Tables 5, 6, 7, 8 and 9 which are suitable for diagnostic purposes. When a proprietary fragment or a public database sequence is selected for its specificity and ubiquity, it increases the probability that subsets thereof will also be specific and ubiquitous.

The proprietary DNA fragments have been obtained as a repertory of sequences created by amplifying MRSA nucleic acids with new primers. These primers and the repertory of nucleic acids as well as the repertory of nucleotide sequences are further objects of this invention (Tables 4, 5, 6, 7, 8 and 9).

Claims therefore are in accordance with the present invention.

SEQUENCES FOR DETECTION AND IDENTIFICATION OF MRSA

In the description of this invention, the terms «nucleic acids» and «sequences» might be used interchangeably. However, «nucleic acids» are chemical entities while «sequences» are the pieces of information encoded by these «nucleic acids». Both nucleic acids and sequences are equivalently valuable sources of information for the matter pertaining to this invention.

Oligonucleotide primers and probes design and synthesis

As part of the design rules, all oligonucleotides (probes for hybridization and primers for DNA amplification by PCR) were evaluated for their suitability for hybridization or PCR amplification by computer analysis using standard programs (i.e. the GCG Wisconsin package programs, the primer analysis software Oligo™ 6 and MFOLD 3.0). The potential suitability of the PCR primer pairs was also evaluated prior to their synthesis by verifying the absence of unwanted features such as long stretches of one nucleotide and a high proportion of G or C residues at the 3' end (Persing *et al.*, 1993, Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.). Oligonucleotide amplification primers were synthesized using an automated DNA synthesizer (Applied Biosystems). Molecular beacon designs were evaluated using criteria established by Kramer *et al.* (<http://www.molecular-beacons.org>).

The oligonucleotide sequence of primers or probes may be derived from either strand of the duplex DNA. The primers or probes may consist of the bases A, G, C, or T or analogs and they may be degenerated at one or more chosen nucleotide position(s) (Nichols *et al.*, 1994, Nature **369**:492-493). Primers and probes may also consist of nucleotide analogs such as Locked Nucleic Acids (LNA) (Koskinen

al., 1998, Tetrahedron **54**:3607-3630), and Peptide Nucleic Acids (PNA) (Egholm *et al.*, 1993, Nature **365**:566-568). The primers or probes may be of any suitable length and may be selected anywhere within the DNA sequences from proprietary fragments, or from selected database sequences which are suitable for the detection
5 of MRSA.

Variants for a given target microbial gene are naturally occurring and are attributable to sequence variation within that gene during evolution (Watson *et al.*, 1987, Molecular Biology of the Gene, 4th ed., The Benjamin/Cummings Publishing
10 Company, Menlo Park, CA; Lewin, 1989, Genes IV, John Wiley & Sons, New York, NY). For example, different strains of the same microbial species may have a single or more nucleotide variation(s) at the oligonucleotide hybridization site. The person skilled in the art is well aware of the existence of variant nucleic acids and/or sequences for a specific gene and that the frequency of sequence variations
15 depends on the selective pressure during evolution on a given gene product. The detection of a variant sequence for a region between two PCR primers may be demonstrated by sequencing the amplification product. In order to show the presence of sequence variations at the primer hybridization site, one has to amplify a larger DNA target with PCR primers outside that hybridization site. Sequencing
20 of this larger fragment will allow the detection of sequence variation at this primer hybridization site. A similar strategy may be applied to show variations at the hybridization site of a probe. Insofar as the divergence of the target nucleic acids and/or sequences or a part thereof does not affect significantly the sensitivity and/or specificity and/or ubiquity of the amplification primers or probes, variant
25 microbial DNA is under the scope of this invention. Variants of the selected primers or probes may also be used to amplify or hybridize to a variant target DNA.

DNA amplification

For DNA amplification by the widely used PCR method, primer pairs were derived from our proprietary DNA fragments or from public database sequences.

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During DNA amplification by PCR, two oligonucleotide primers binding respectively to each strand of the heat-denatured target DNA from the microbial genome are used to amplify exponentially *in vitro* the target DNA by successive thermal cycles allowing denaturation of the DNA, annealing of the primers and
10 synthesis of new targets at each cycle (Persing *et al.*, 1993, Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.).

Briefly, the PCR protocols on a standard thermocycler (PTC-200 from MJ
15 Research Inc., Watertown, MA) were as follows: Treated standardized bacterial suspensions or genomic DNA prepared from bacterial cultures or clinical specimens were amplified in a 20 µl PCR reaction mixture. Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 2.5 mM MgCl₂, 0.4 µM of each primer, 200 µM of each of the four dNTPs (Pharmacia Biotech), 3.3 µg/µl bovine
20 serum albumin (BSA) (Sigma-Aldrich Canada Ltd, Oakville, Ontario, Canada) and 0.5 unit of *Taq* DNA polymerase (Promega Corp., Madison, WI) combined with the *TaqStart*TM antibody (BD Biosciences, Palo Alto, CA). The *TaqStart*TM antibody, which is a neutralizing monoclonal antibody to *Taq* DNA polymerase, was added to all PCR reactions to enhance the specificity and the sensitivity of the
25 amplifications (Kellogg *et al.*, 1994, Biotechniques 16:1134-1137). The treatment of bacterial cultures or of clinical specimens consists in a rapid protocol to lyse the microbial cells and eliminate or neutralize PCR inhibitors (described in co-pending application US 60/306,163). For amplification from purified genomic DNA, the samples were added directly to the PCR amplification mixture. An internal control,

derived from sequences not found in the target MREJ sequences or in the human genome, was used to verify the efficiency of the PCR reaction and the absence of significant PCR inhibition.

- 5 The number of cycles performed for the PCR assays varies according to the sensitivity level required. For example, the sensitivity level required for microbial detection directly from a clinical specimen is higher than for detection from a microbial culture. Consequently, more sensitive PCR assays having more thermal cycles are probably required for direct detection from clinical specimens.

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- The person skilled in the art of nucleic acid amplification knows the existence of other rapid amplification procedures such as ligase chain reaction (LCR), reverse transcriptase PCR (RT-PCR), transcription-mediated amplification (TMA), self-sustained sequence replication (3SR), nucleic acid sequence-based amplification (NASBA), strand displacement amplification (SDA), branched DNA (bDNA),
15 cycling probe technology (CPT), solid phase amplification (SPA), rolling circle amplification technology (RCA), solid phase RCA, anchored SDA and nuclease dependent signal amplification (NDSA) (Lee *et al.*, 1997, Nucleic Acid Amplification Technologies: Application to Disease Diagnosis, Eaton Publishing,
20 Boston, MA; Persing *et al.*, 1993, Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.; Westin *et al.*, 2000, Nat. Biotechnol. 18:199-204). The scope of this invention is not limited to the use of amplification by PCR, but rather includes the use of any nucleic acid amplification method or any other procedure which may be used to
25 increase the sensitivity and/or the rapidity of nucleic acid-based diagnostic tests. The scope of the present invention also covers the use of any nucleic acids amplification and detection technology including real-time or post-amplification detection technologies, any amplification technology combined with detection, any hybridization nucleic acid chips or array technologies, any amplification chips or

combination of amplification and hybridization chip technologies. Detection and identification by any nucleotide sequencing method is also under the scope of the present invention.

- 5 Any oligonucleotide derived from the *S. aureus* MREJ DNA sequences and used with any nucleic acid amplification and/or hybridization technologies are also under the scope of this invention.

Evaluation of the MRSA detection method developed by Hiramatsu *et al.*

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According to Hiramatsu *et al.* (Ito *et al.*, 1999, Antimicrob. Agents Chemother. **43**:1449-1458; Katayama *et al.*, 2000, Antimicrob. Agents Chemother. **44**:1549-1555; Ito *et al.*, 2001, Antimicrob. Agents Chemother. **45**:1323-1336, Ma *et al.*, 2002, Antimicrob. Agents Chemother. **46**:1147-1152), four types of SCCmec DNA
15 are found among MRSA strains. They have found that SCCmec DNAs are integrated at a specific site of the MSSA chromosome (named *orfX*). They developed a MRSA-specific multiplex PCR assay including primers that can hybridize to the right extremity of SCCmec types I, II and III (SEQ ID NOs.: 18, 19, 20, 21, 22, 23, 24 in US patent 6,156,507 corresponding to SEQ IDNOs.: 52,
20 53, 54, 55, 56, 57, 58, respectively, in the present invention) as well as primers specific to the *S. aureus* chromosome to the right of the SCCmec integration site (SEQ ID NO.: 25, 28, 27, 26, 29 in US patent 6,156,507 corresponding to SEQ ID NOs.: 59, 60, 61, 62, 63, respectively, in the present invention) (Table 1 and Figure 1). The set of primers described by Hiramatsu *et al.* as being the optimal primer
25 combination (SEQ ID NOs.: 22, 24 and 28 in US patent 6,156,507 corresponding to SEQ ID NOs.: 56, 58 and 60 in the present invention) was used in the present invention to test by PCR a variety of MRSA, MSSA, methicillin-resistant CNS (MRCNS) and methicillin-sensitive CNS (MSCNS) strains (Table 2). A PCR assay performed using a standard thermocycler (PTC-200 from MJ Research Inc.) was

used to test the ubiquity, the specificity and the sensitivity of these primers using the following protocol: one μ l of a treated standardized bacterial suspension or of a genomic DNA preparation purified from bacteria were amplified in a 20 μ l PCR reaction mixture. Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 2.5 mM MgCl₂, 0.4 μ M of each of the SCCmec- and *S. aureus* chromosome-specific primers (SEQ ID NOs.: 22, 24 and 28 in US patent 6,156,507 corresponding to SEQ ID NOs.: 56, 58 and 60 in the present invention), 200 μ M of each of the four dNTPs (Pharmacia Biotech), 3.3 μ g/ μ l BSA (Sigma), and 0.5 U *Taq* polymerase (Promega) coupled with *TaqStart*TM Antibody (BD Biosciences).

PCR reactions were then subjected to thermal cycling 3 min at 94°C followed by 40 cycles of 60 seconds at 95°C for the denaturation step, 60 seconds at 55°C for the annealing step, and 60 seconds at 72°C for the extension step, then followed by a terminal extension of 7 minutes at 72°C using a standard thermocycler (PTC-200 from MJ Research Inc.). Detection of the PCR products was made by electrophoresis in agarose gels (2 %) containing 0.25 μ g/ml of ethidium bromide. Twenty of the 39 MRSA strains tested were not amplified with the PCR assay developed by Hiramatsu *et al.* (Example 1, Tables 2 and 3).

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With a view of establishing a rapid diagnostic test for MRSA, the present inventors developed new sets of primers specific to the right extremity of SCCmec types I and II (SEQ ID NOs.: 66, 100 and 101) (Annex 1), SCCmec type II (SEQ ID NOs.: 97 and 99), SCCmec type III (SEQ ID NOs.: 67, 98 and 102) and in the *S. aureus* chromosome to the right of the SCCmec integration site (SEQ ID NOs.: 64, 70, 71, 72, 73, 74, 75 and 76) (Table 5). These primers, amplifying short amplicons (171 to 278 bp), are compatible for use in rapid PCR assays (Table 7). The design of these primers was based on analysis of multiple sequence alignments of *orfX* and SCCmec sequences described by Hiramatsu *et al.* (US patent

6,156,507) or available from GenBank (Table 10, Annex I). These different sets of primers were used to test by PCR a variety of MRSA, MSSA, MRCNS and MSCNS strains. Several amplification primers were developed to detect all three SCCmec types (SEQ ID NOs.: 97 and 99 for SCCmec type II, SEQ ID NOs.: 66, 100 and 101 for SCCmec types I and II and SEQ ID NOs.: 67, 98 and 102 for SCCmec type III). Primers were chosen according to their specificity for MRSA strains, their analytical sensitivity in PCR and the length of the PCR product. A set of two primers was chosen for the SCCmec right extremity region (SEQ ID NO.: 66 specific to SCCmec types I and II; SEQ ID NO.: 67 specific to SCCmec type III). Of the 8 different primers designed to anneal on the *S. aureus* chromosome to the right of the SCCmec integration site (targeting *orfX* gene) (SEQ ID NOs.: 64, 70, 71, 72, 73, 74, 75 and 76), only one (SEQ ID.: 64) was found to be specific for MRSA based on testing with a variety of MRSA, MSSA, MRCNS and MSCNS strains (Table 12). Consequently, a PCR assay using the optimal set of primers (SEQ ID NOs.: 64, 66 and 67) which could amplify specifically MRSA strains containing SCCmec types I, II and III was developed (Figure 2, Annex I). While the PCR assay developed with this novel set of primers was highly sensitive (i.e. allowed the detection of 2 to 5 copies of genome for all three SCCmec types) (Table 11), it had the same shortcomings (i.e. lack of ubiquity) of the test developed by Hiramatsu et al. The 20 MRSA strains which were not amplified by the Hiramatsu et al. primers were also not detected by the set of primers comprising SEQ ID NOs.: 64, 66 and 67 (Tables 3 and 12). Clearly, diagnostic tools for achieving at least 50% ubiquity amongst the tested strains are needed.

With a view to establish a more ubiquitous (i.e. ability to detect all or most MRSA strains) detection and identification method for MRSA, we determined the sequence of the MREJ present in these 20 MRSA strains which were not amplified. This research has led to the discovery and identification of seven novel distinct MREJ target sequences which can be used for diagnostic purposes. These

seven new MREJ sequences could not have been predicted nor detected with the system described in US patent 6,156,507 by Hiramatsu *et al.* Namely, the present invention represents an improved method for the detection and identification of MRSA because it provides a more ubiquitous diagnostic method which allows for the detection of all major epidemic MRSA clones from around the world.

Sequencing of MREJ nucleotide sequences from MRSA strains not amplifiable with primers specific to SCCmec types I, II and III

Since DNA from twenty MRSA strains were not amplified with the set of primers developed by Hiramatsu *et al.* (SEQ ID NOs.: 22, 24 and 28 in US patent 6,156,507 corresponding to SEQ ID NOs.: 56, 58 and 60 in the present invention) (Tables 2 and 3) nor with the set of primers developed in the present invention based on the same three SCCmec types (I, II and III) sequences (SEQ ID NOs.: 64, 66 and 67) (Table 12), the nucleotide sequence of the MREJ was determined for sixteen of these twenty MRSA strains.

Transposase of IS431 is often associated with the insertion of resistance genes within the *mec* locus. The gene encoding this transposase has been described frequently in one or more copies within the right segment of SCCmec (Oliveira *et al.*, 2000, Antimicrob. Agents Chemother. **44**:1906-1910; Ito *et al.*, 2001, Antimicrob. Agents Chemother. **45**:1323-36). Therefore, in a first attempt to sequence the novel MREJ for 16 of the 20 MRSA strains described in Table 3, a primer was designed in the sequence of the gene coding for the transposase of IS431 (SEQ ID NO.: 68) and combined with an *orfX*-specific primer to the right of the SCCmec integration site (SEQ ID NO.: 70) (Tables 5 and 8). The strategy used to select these primers is illustrated in Figure 3.

The MREJ fragments to be sequenced were amplified using the following amplification protocol: one μL of treated cell suspension (or of a purified genomic DNA preparation) was transferred directly into 4 tubes containing 39 μL of a PCR reaction mixture. Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 2.5 mM MgCl_2 , 1 μM of each of the 2 primers (SEQ ID NOs.: 68 and 70), 200 μM of each of the four dNTPs, 3.3 $\mu\text{g}/\mu\text{L}$ of BSA (Sigma-Aldrich Canada Ltd) and 0.5 unit of *Taq* DNA polymerase (Promega) coupled with the *TaqStart*TM Antibody (BD Biosciences). PCR reactions were submitted to cycling using a standard thermocycler (PTC-200 from MJ Research Inc.) as follows: 3 min at 94 °C followed by 40 cycles of 5 sec at 95 °C for the denaturation step, 30 sec at 55 °C for the annealing step and 2 min at 72 °C for the extension step.

Subsequently, the four PCR-amplified mixtures were pooled and 10 μL of the mixture were resolved by electrophoresis in a 1.2% agarose gel containing 0.25 $\mu\text{g}/\text{mL}$ of ethidium bromide. The amplicons were then visualized with an Alpha-Imager (Alpha Innotech Corporation, San Leandro, CA) by exposing to UV light at 254 nm. Amplicon size was estimated by comparison with a 1 kb molecular weight ladder (Life Technologies, Burlington, Ontario, Canada). The remaining PCR-amplified mixture (150 μL , total) was also resolved by electrophoresis in a 1.2% agarose gel. The amplicons were then visualized by staining with methylene blue (Flores *et al.*, 1992, Biotechniques, 13:203-205). Amplicon size was once again estimated by comparison with a 1 kb molecular weight ladder. Of the sixteen strains selected from the twenty described in Table 3, six were amplified using SEQ ID NOs.: 68 and 70 as primers (CCRI-178, CCRI-8895, CCRI-8903, CCRI-1324, CCRI-1331 and CCRI-9504). For these six MRSA strains, an amplification product of 1.2 kb was obtained. The band corresponding to this specific amplification product was excised from the agarose gel and purified using the QIAquickTM gel extraction kit (QIAGEN Inc., Chatsworth, CA). The gel-

purified DNA fragment was then used directly in the sequencing protocol. Both strands of the MREJ amplification products were sequenced by the dideoxynucleotide chain termination sequencing method by using an Applied Biosystems automated DNA sequencer (model 377) with their Big Dye™

5 Terminator Cycle Sequencing Ready Reaction Kit (Applied Biosystems, Foster City, CA). The sequencing reactions were performed by using the same primers (SEQ ID NOs.: 68 and 70) and 10 ng/100 bp per reaction of the gel-purified amplicons. Sequencing of MREJ from the six MRSA strains (CCRI-178, CCRI-8895, CCRI-8903, CCRI-1324, CCRI-1331 and CCRI-9504) described in Table 3
10 yielded SEQ ID NOs.: 42, 43, 44, 45, 46 and 51, respectively (Table 4).

In order to ensure that the determined sequence did not contain errors attributable to the sequencing of PCR artefacts, we have sequenced two preparations of the gel-purified MREJ amplification products originating from two independent PCR
15 amplifications. For most target fragments, the sequences determined for both amplicon preparations were identical. Furthermore, the sequences of both strands were 100% complementary thereby confirming the high accuracy of the determined sequence. The MREJ sequences determined using the above strategy are described in the Sequence Listing and in Table 4.

20

In order to sequence MREJ in strains for which no amplicon had been obtained using the strategy including primers specific to the transposase gene of *IS431* and *orfX*, another strategy using primers targeting *mecA* and *orfX* sequences was used to amplify longer genomic fragments. A new PCR primer targeting *mecA* (SEQ ID
25 NO.: 69) (Table 8) to be used in combination with the same primer in the *orfX* sequence (SEQ ID NO.: 70). The strategy used to select these primers is illustrated in Figure 3.

The following amplification protocol was used: Purified genomic DNA (300 ng) was transferred to a final volume of 50 µl of a PCR reaction mixture. Each PCR reaction contained 1X *Herculase* buffer (Stratagene, La Jolla, CA), 0.8 µM of each of the 2 primers (SEQ ID NOs.: 69 and 70), 0.56 mM of each of the four dNTPs and 5 units of *Herculase* (Stratagene). PCR reactions were subjected to cycling using a standard thermal cycler (PTC-200 from MJ Research Inc.) as follows: 2 min at 92 °C followed by 35 or 40 cycles of 10 sec at 92 °C for the denaturation step, 30 sec at 55 °C for the annealing step and 30 min at 68 °C for the extension step.

Subsequently, 10 µL of the PCR-amplified mixture were resolved by electrophoresis in a 0.7% agarose gel containing 0.25 µg/mL of ethidium bromide. The amplicons were then visualized as described above. Amplicon size was estimated by comparison with a 1 kb molecular weight ladder (Life Technologies).

A reamplification reaction was then performed in 2 to 5 tubes using the same protocol with 3 µl of the first PCR reaction used as test sample for the second amplification. The PCR-reamplified mixtures were pooled and also resolved by electrophoresis in a 0.7% agarose gel. The amplicons were then visualized by staining with methylene blue as described above. An amplification product of approximately 12 kb was obtained using this amplification strategy for all strains tested. The band corresponding to the specific amplification product was excised from the agarose gel and purified as described above. The gel-purified DNA fragment was then used directly in the sequencing protocol as described above. The sequencing reactions were performed by using the same amplification primers (SEQ ID NOs.: 69 and 70) and 425-495 ng of the gel-purified amplicons per reaction. Subsequently, internal sequencing primers (SEQ ID NOs.: 65, 77 and 96) (Table 8) were used to obtain sequence data on both strands for a larger portion of the amplicon. Five of the 20 MRSA strains (CCRI-1331, CCRI-1263, CCRI-1377, CCRI-1311 and CCRI-2025) described in Table 3 were sequenced using this

strategy, yielding SEQ ID NOs.: 46, 47, 48, 49 and 50, respectively (Table 4). Sequence within *mecA* gene was also obtained from the generated amplicons yielding SEQ ID NOs: 27, 28, 29, 30 and 31 from strains CCRI-2025, CCRI-1263, CCRI-1311, CCRI-1331 and CCRI-1377, respectively (Table 4). Longer
5 sequences within the *mecA* gene and from downstream regions were also obtained for strains CCRI-2025, CCRI-1331, and CCRI-1377 as described below.

In order to obtain longer sequences of the *orfX* gene, two other strategies using primers targeting *mecA* and *orfX* sequences (at the start codon) was used to amplify
10 longer chromosome fragments. A new PCR primer was designed in *orfX* (SEQ ID NO.: 132) to be used in combination with the same primer in the *mecA* gene (SEQ ID NO.: 69). The strategy used to select these primers is illustrated in Figure 3. Eight *S. aureus* strains were amplified using primers SEQ ID NOs.: 69 and 132 (CCRI-9860, CCRI-9208, CCRI-9504, CCRI-1331, CCRI-9583, CCRI-9681,
15 CCRI-2025 and CCRI-1377). The strategy used to select these primers is illustrated in Figure 3.

The following amplification protocol was used: Purified genomic DNA (350 to 500 ng) was transferred to a 50 µl PCR reaction mixture. Each PCR reaction
20 contained 1X Herculase buffer (Stratagene), 0.8 µM of each of the set of 2 primers (SEQ ID NOs.: 69 and 132), 0.56 mM of each of the four dNTPs and 7.5 units of *Herculase* (Stratagene) with 1 mM MgCl₂. PCR reactions were subjected to thermocycling as described above.

25 Subsequently, 5 µL of the PCR-amplified mixture were resolved by electrophoresis in a 0.8% agarose gel containing 0.25 µg/mL of ethidium bromide. The amplicons were then visualized as described above. For one *S. aureus* strain (CCRI-9583), a reamplification was then performed by using primers SEQ ID NOs.: 96 and 158 (Figure 3) in 4 tubes, using the same PCR protocol, with 2 µl of

the first PCR reaction as test sample for the second amplification. The PCR-reamplified mixtures were pooled and also resolved by electrophoresis in a 0.8% agarose gel. The amplicons were then visualized by staining with methylene blue as described above. A band of approximately 12 to 20 kb was obtained using this
5 amplification strategy depending on the strains tested. The band corresponding to the specific amplification product was excised from the agarose gel and purified using the QIAquick™ gel extraction kit or QIAEX II gel extraction kit (QIAGEN Inc.). Two strains, CCRI-9583 and CCRI-9589, were also amplified with primers SEQ ID NOs.: 132 and 150, generating an amplification product of 1.5 kb. Long
10 amplicons (12-20 kb) were sequenced using 0.6 to 1 µg per reaction, while short amplicons (1.5 kb) were sequenced using 150 ng per reaction. Sequencing reactions were performed using different sets of primers for each *S. aureus* strain:
1) SEQ ID NOs.: 68, 70, 132, 145, 146, 147, 156, 157 and 158 for strain CCRI-9504; 2) SEQ ID NOs.: 70, 132, 154 and 155 for strain CCRI-2025; 3) SEQ ID
15 NOs.: 70, 132, 148, 149, 158 and 159 for strain CCRI-9681; 4) SEQ ID NOs.: 70, 132, 187, and 188 for strain CCRI-9860; 5) SEQ ID NOs.: 70, 132, 150 and 159 for strain CCRI-9589, 6) SEQ ID NOs.: 114, 123, 132, 150 and 158 for strain CCRI-9583; 7) SEQ ID NOs.: 70, 132, 154 and 155 for strain CCRI-1377, 8) SEQ ID NOs.: 70, 132, 158 and 159 for strain CCRI-9208; 9) SEQ ID NOs.: 68, 70, 132,
20 145, 146, 147 and 158 for strain CCRI-1331; and 10) SEQ ID NOs.: 126 and 127 for strain CCRI-9770.

In one strain (CCRI-9770), the *orfX* and *orfSA0022* genes were shown to be totally or partially deleted based on amplification using primers specific to these genes
25 (SEQ ID NOs.: 132 and 159 and SEQ ID NOs.: 128 and 129, respectively) (Table 8). Subsequently, a new PCR primer was designed in *orfSA0021* (SEQ ID NO.: 126) to be used in combination with the same primer in the *mecA* gene (SEQ ID NO.: 69). An amplification product of 4.5 kb was obtained with this primer set.

Amplification, purification of amplicons and sequencing of amplicons were performed as described above.

To obtain the sequence of the *SSCmec* region containing *mecA* for ten of the 20
5 MRSA strains described in Table 3 (CCRI-9504, CCRI-2025, CCRI-9208, CCRI-1331, CCRI-9681, CCRI-9860, CCRI-9770, CCRI-9589, CCRI-9583 and CCRI-1377), the primer described above designed in *mecA* (SEQ ID NO.: 69) was used in combination with a primer designed in the downstream region of *mecA* (SEQ ID NO.: 118) (Table 8). An amplification product of 2 kb was obtained for all the
10 strains tested. For one strain, CCRI-9583, a re-amplification with primers SEQ ID NOs.: 96 and 118 was performed with the amplicon generated with primers SEQ ID NOs.: 69 and 132 described above. The amplification, re-amplification, purification of amplicons and sequencing reactions were performed as described above. Sequencing reactions were performed with amplicons generated with SEQ
15 ID NOs.: 69 and 132 described above or SEQ ID NOs.: 69 and 118. Different sets of sequencing primers were used for each *S. aureus* strain: 1) SEQ ID NOs.: 69, 96, 117, 118, 120, 151, 152 for strains CCRI-9504, CCRI-2025, CCRI-1331, CCRI-9770 and CCRI-1377; 2) SEQ ID NOs.: 69, 96, 118 and 120 for strains CCRI-9208, CCRI-9681 and CCRI-9589; 3) SEQ ID NOs.: 69, 96, 117, 118, 120
20 and 152 for strain CCRI-9860; and 4) SEQ ID NOs.: 96, 117, 118, 119, 120, 151 and 152 for strain CCRI-9583.

The sequences obtained for 16 of the 20 strains non-amplifiable by the Hiramatsu
assay (Table 4) were then compared to the sequences available from public
25 databases. In all cases, portions of the sequence had an identity close to 100% to publicly available sequences for *orfX* (SEQ ID NOs.: 42-51, 165-168 and 171) or *mecA* and downstream region (SEQ ID NOs.: 27-31, 189-193, 195, 197-199 and 225). However, while the *orfX* portion of the fragments (SEQ ID NOs.: 42-51, 165-168 and 171) shared nearly 100% identity with the *orfX* gene of MSSA strain

NCTC 8325 described by Hiramatsu *et al.* (SEQ ID NO.: 3), the DNA sequence within the right extremity of *SCCmec* itself was shown to be very different from those of types I, II, III and IV described by Hiramatsu *et al.* (Table 13, Figure 4). Six different novel sequence types were obtained.

5

It should be noted that Hiramatsu *et al.* demonstrated that *SCCmec* type I could be associated with MREP type i, *SCCmec* types II and IV are associated with MREP type ii, and *SCCmec* type III is associated with MREP type iii. Our MREJ sequencing data from various MRSA strains led to the discovery of 6 novel MREP types designated types iv, v, vi, vii, viii, and ix. The MREJ comprising distinct MREP types were named according to the MREP numbering scheme. Hence, MREP type i is comprised within MREJ type i, MREP type ii is comprised within MREJ type ii and so on up to MREP type ix.

10

15 The sequences within the right extremity of *SCCmec* obtained from strains CCRI-178, CCRI-8895, CCRI-8903, CCRI-1324, CCRI-1331 and CCRI-9504 (SEQ ID NOs.: 42, 43, 44, 45, 46 and 51) were nearly identical to each other and exhibited nearly 100% identity with *IS431* (GenBank accession numbers AF422691, ABO37671, AF411934). However, our sequence data revealed for the first time
20 the location of this *IS431* sequence at the right extremity of *SCCmec* adjacent to the integration site. Therefore, as the sequences at the right extremity of *SCCmec* from these 6 MRSA strains were different from those of *SCCmec* type I from strain NCTC 10442, *SCCmec* type II from strain N315, *SCCmec* type III from strain 85/2082 and *SCCmec* type IV from strains CA05 and 8/6-3P described by
25 Hiramatsu *et al.* (Ito *et al.*, 2001, *Antimicrob. Agents Chemother.* **45**:1323-1336; Ma *et al.*, 2002, *Antimicrob. Agents Chemother.* **46**:1147-1152), these new sequences were designated as MREP type iv (SEQ ID NOs.: 42-46 and 51). A BLAST search with the *SCCmec* portion of MREP type iv sequences produced significant alignments with sequences coding for portions of a variety of known

transposases. For example, when compared to Genbank accession no. AB037671, MREP type iv from SEQ ID NO. 51 shared 98% identity with the putative transposase of IS431 and its downstream region; two gaps of 7 nucleotides each were also present in the alignment.

- 5 Sequences obtained from strains CCRI-1263, CCRI-1377, CCRI-1311 and CCRI-2025 (SEQ ID NOs.: 47-50) were nearly identical to each other and different from all three SCC*mec* types and MREP type iv and, consequently, were designated as MREP type v. When compared with Genbank sequences using BLAST, MREP type v sequences did not share any significant homology with any published
10 sequence, except for the first 28 nucleotides. That short stretch corresponded to the last 11 coding nucleotides of *orfX*, followed by the 17 nucleotides downstream, including the right inverted repeat (IR-R) of SCC*mec*.

Sequence obtained from strain CCRI-9208 was also different from all three SCC*mec* types and MREP types iv and v and, consequently, was designated as
15 MREP type vi (SEQ ID NO.: 171). Upon a BLAST search, MREP type vi was shown to be unique, exhibiting no significant homology to any published sequence.

Sequences obtained from strains CCRI-9583 and CCRI-9589 were also different from all three SCC*mec* types and MREP types iv to vi and were therefore
20 designated as MREP type vii (SEQ ID NOs.: 165 and 166). Upon a BLAST search, MREP type vii was also shown to be unique, exhibiting no significant homology to any published sequence.

Sequence obtained from strain CCRI-9860 was also different from all three SCC*mec* types and MREP types iv to vii and was therefore designated as MREP
25 type viii (SEQ ID NO.: 167). Sequence obtained from strain CCRI-9681 was also different from all three SCC*mec* types and MREP types iv to viii and was therefore designated as MREP type ix (SEQ ID NO.: 168). BLAST searches with the SCC*mec* portion of MREP types viii and ix sequences yielded significant alignments, but only for the first ~150 nucleotides of each MREP type. For

example, the beginning of the MREP type viii sequence had 88% identity with a portion of Genbank accession no. AB063173, but no significant homology with any published sequence was found for the rest of the sequence. In the same manner, the first ~150 nucleotides of MREP type ix had 97% identity with the same portion of AB063173, with the rest of the sequence being unique. The short homologous portion of MREP types viii and ix corresponds in AB063173 to the last 14 coding nucleotides of *orfX*, the IR-R of *SCCmec*, and a portion of *orfCM009*. Although sharing resemblances, MREP types viii and ix are very different from one another; as shown in Table 13, there is only 55.2% identity between both types for the first 500 nucleotides of the *SCCmec* portion.

Finally, we did not obtain any sequence within *SSCmec* from strain CCRI-9770. However, as described in the section "Sequencing of MREJ nucleotide sequences from MRSA strains not amplifiable with primers specific to *SCCmec* types I, II and III", this strain has apparently a partial or total deletion of the *orfX* and *orfSA0022* genes in the chromosomal DNA to the right of the *SCCmec* integration site and this would represent a new right extremity junction. We therefore designated this novel sequence as MREP type x (SEQ ID NO.: 172). Future sequencing should reveal whether this so called MREJ type x contains a novel MREP type x or if the lack of amplification is indeed caused by variation in the chromosomal part of the MREJ.

The sequences of the first 500-nucleotide portion of the right extremity of all *SCCmec* obtained in the present invention were compared to those of *SCCmec* types I, II and III using GCG programs Pileup and Gap. Table 13 depicts the identities at the nucleotide level between *SCCmec* right extremities of the six novel sequences with those of *SCCmec* types I, II and III using the GCG program Gap. While *SCCmec* types I and II showed nearly 79.2% identity (differing only by a 102 bp insertion present in *SCCmec* type II) (Figures 1, 2 and 4), all other MREP types showed identities varying from 40.9 to 57.1%. This explains why the right

extremities of the novel MREP types iv to ix disclosed in the present invention could not have been predicted nor detected with the system described by Hiramatsu *et al.*

- 5 Four strains (CCRI-1312, CCRI-1325, CCRI-9773 and CCRI-9774) described in Table 3 were not sequenced but rather characterized using PCR primers. Strains CCRI-1312 and CCRI-1325 were shown to contain MREP type v using specific amplification primers described in Examples 4, 5 and 6 while strains CCRI-9773 and CCRI-9774 were shown to contain MREP type vii using specific amplification
10 primers described in Example 7.

To obtain the complete sequence of the SCC*mec* present in the MRSA strains described in the present invention, primers targeting the *S. aureus* chromosome to the left (upstream of the *mecA* gene) of the SCC*mec* integration site were
15 developed. Based on available public database sequences, 5 different primers were designed (SEQ ID NOs.: 85-89) (Table 9). These primers can be used in combination with *S. aureus* chromosome-specific primers in order to sequence the entire SCC*mec* or, alternatively, used in combination with a *mecA*-specific primer (SEQ ID NO.: 81) in order to sequence the left extremity junction of SCC*mec*. We
20 have also developed several primers specific to known SCC*mec* sequences spread along the locus in order to obtain the complete sequence of SCC*mec* (Table 9). These primers will allow to assign a SCC*mec* type to the MRSA strains described in the present invention.

25 **Selection of amplification primers from SCC*mec*/orfX sequences**

The MREJ sequences determined by the inventors or selected from public databases were used to select PCR primers for detection and identification of

MRSA. The strategy used to select these PCR primers was based on the analysis of multiple sequence alignments of various MREJ sequences.

Upon analysis of the six new MREP types iv to ix sequence data described above,
5 primers specific to each new MREP type sequence (SEQ ID NOs.: 79, 80, 109, 112, 113, 115, 116 and 204) were designed (Figure 2, Table 5, Examples 3, 4, 5, 6, 7 and 8). Primers specific to MREP types iv, v and vii (SEQ ID NOs.: 79, 80 and 112) were used in multiplex with the three primers to detect SCCmec types I, II and III (SEQ ID NOs: 64, 66 and 67) and the primer specific to the *S. aureus orfX*
10 (SEQ ID NO. 64) (Examples 3, 4, 5, 6 and 7). Primers specific to MREP types vi, viii and ix (SEQ ID NOs.: 204, 115, 116 and 109) were also designed and tested against their specific target (Example 8).

Detection of amplification products

15

Classically, the detection of PCR amplification products is performed by standard ethidium bromide-stained agarose gel electrophoresis as described above. It is however clear that other methods for the detection of specific amplification products, which may be faster and more practical for routine diagnosis, may be
20 used. Examples of such methods are described in co-pending patent application WO01/23604 A2.

Amplicon detection may also be performed by solid support or liquid hybridization using species-specific internal DNA probes hybridizing to an amplification
25 product. Such probes may be generated from any sequence from our repertory and designed to specifically hybridize to DNA amplification products which are objects of the present invention. Alternatively, amplicons can be characterized by sequencing. See co-pending patent application WO01/23604 A2 for examples of detection and sequencing methods.

In order to improve nucleic acid amplification efficiency, the composition of the reaction mixture may be modified (Chakrabarti and Schutt, 2002, Biotechniques, 32:866-874; Al-Soud and Radstrom, 2002, J. Clin. Microbiol., 38:4463-4470; Al-Soud and Radstrom, 1998, Appl. Environ. Microbiol., 64:3748-3753; Wilson, 1997, Appl. Environ. Microbiol., 63:3741-3751). Such modifications of the amplification reaction mixture include the use of various polymerases or the addition of nucleic acid amplification facilitators such as betaine, BSA, sulfoxides, protein gp32, detergents, cations, tetramethylammonium chloride and others.

In a preferred embodiment, real-time detection of PCR amplification was monitored using molecular beacon probes in a SmartCycler[®] apparatus (Cepheid, Sunnyvale, CA). A multiplex PCR assay containing primers specific to MREP types i to v and *orfX* of *S. aureus* (SEQ ID NOs.: 64, 66, 67, 79 and 80), a molecular beacon probe specific to the *orfX* sequence (SEQ ID NO. 84, see Annex II and Figure 2) and an internal control to monitor PCR inhibition was developed. The internal control contains sequences complementary to MREP type iv- and *orfX*-specific primers (SEQ ID NOs. 79 and 64). The assay also contains a molecular beacon probe labeled with tetrachloro-6-carboxyfluorescein (TET) specific to sequence within DNA fragment generated during amplification of the internal control. Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 3.45 mM MgCl₂, 0.8 µM of each of the MREP-specific primers (SEQ ID NOs.: 66 and 67) and *orfX*-specific primer (SEQ ID NO.: 64), 0.4 µM of each of the MREP-specific primers (SEQ ID NOs.: 79 and 80), 80 copies of the internal control, 0.2 µM of the TET-labeled molecular beacon probe specific to the internal control, 0.2 µM of the molecular beacon probe (SEQ ID NO.: 84) labeled with 6-carboxyfluorescein (FAM), 330 µM of each of the four dNTPs (Pharmacia Biotech), 3.45 µg/µl of BSA (Sigma), and 0.875 U *Taq* polymerase (Promega) coupled with *TaqStart*[™] Antibody (BD Biosciences). The PCR

amplification on the Smart Cycler[®] was performed as follows: 3 min. at 95°C for initial denaturation, then forty-eight cycles of three steps consisting of 5 seconds at 95°C for the denaturation step, 15 seconds at 60°C for the annealing step and 15 seconds at 72°C for the extension step. Sensitivity tests performed by using
5 purified genomic DNA from one MRSA strain of each MREP type (i to v) showed a detection limit of 2 to 10 genome copies (Example 5). None of the 26 MRCNS or 10 MSCNS tested were positive with this multiplex assay. The eight MRSA strains (CCRI-9208, CCRI-9770, CCRI-9681, CCRI-9860, CCRI-9583, CCRI-9773, CCRI-9774, CCRI-9589) which harbor the new MREP types vi, viii, ix and x
10 sequences described in the present invention remained undetectable (Example 5).

In a preferred embodiment, detection of MRSA using the real-time multiplex PCR assay on the Smart Cycler[®] apparatus (Cepheid, Sunnyvale, CA) directly from clinical specimens was evaluated. A total of 142 nasal swabs were collected during
15 a MRSA hospital surveillance program at the Montreal General Hospital (Montreal, Quebec, Canada). The swab samples were tested at the Centre de Recherche en Infectiologie de l'Université Laval within 24 hours of collection. Upon receipt, the swabs were plated onto mannitol agar and then the nasal material from the same swab was prepared with a simple and rapid specimen preparation
20 protocol described in co-pending patent application number US 60/306,163. Classical identification of MRSA was performed by standard culture methods.

The PCR assay detected 33 of the 34 samples positive for MRSA based on the culture method. As compared to culture, the PCR assay detected 8 additional
25 MRSA positive specimens for a sensitivity of 97.1 % and a specificity of 92.6 % (Example 6). This multiplex PCR assay represents a rapid and powerful method for the specific detection of MRSA carriers directly from nasal specimens and can be used with any types of clinical specimens such as wounds, blood or blood culture, CSF, etc.

In a preferred embodiment, a multiplex PCR assay containing primers specific to MREP types i, ii, iii, iv, v and vi and orfX of *S. aureus* (SEQ ID NOs.: 66, 67, 79, 80 and 112), and three molecular beacons probes specific to orfX sequence which allowed detection of the two sequence polymorphisms identified in this region of the orfX sequence was developed. Four of the strains which were not detected with the multiplex assay for the detection of MREP types i to v were now detected with this multiplex assay while the four MRSA strains (CCRI-9208, CCRI-9770, CCRI-9681, CCRI-9860) which harbor the MREP types vi, viii, ix and x described in the present invention remained undetectable (Example 7). Primers specific to MREP types vi, viii and ix (SEQ ID NOs.: 204, 115, 116 and 109) were also designed and were shown to detect their specific target strains (Example 8). While the primers and probes derived from the teaching of Hiramatsu *et al.*, permitted the detection of only 48.7% (19 strains out of 39) of the MRSA strains of Table 2, the primers and probes derived from the present invention enable the detection of 97.4 % of the strains (38 strains out of 39) (see examples 7 and 8). Therefore it can be said that our assay has a ubiquity superior to 50% for the MRSA strains listed in Table 2.

Specificity, ubiquity and sensitivity tests for oligonucleotide primers and probes

The specificity of oligonucleotide primers and probes was tested by amplification of DNA or by hybridization with staphylococcal species. All of the staphylococcal species tested were likely to be pathogens associated with infections or potential contaminants which can be isolated from clinical specimens. Each target DNA could be released from microbial cells using standard chemical and/or physical treatments to lyse the cells (Sambrook *et al.*, 1989, Molecular Cloning: A Laboratory Manual, 2nd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY) or alternatively, genomic DNA purified with the GNOME™ DNA kit (Qbiogene, Carlsbad, CA) was used. Subsequently, the DNA was subjected to

amplification with the set of primers. Specific primers or probes hybridized only to the target DNA.

Oligonucleotides primers found to amplify specifically DNA from the target
5 MRSA were subsequently tested for their ubiquity by amplification (i.e. ubiquitous primers amplified efficiently most or all isolates of MRSA). Finally, the analytical sensitivity of the PCR assays was determined by using 10-fold or 2-fold dilutions of purified genomic DNA from the targeted microorganisms. For most assays, sensitivity levels in the range of 2-10 genome copies were obtained. The
10 specificity, ubiquity and analytical sensitivity of the PCR assays were tested either directly with bacterial cultures or with purified bacterial genomic DNA.

Molecular beacon probes were tested using the Smart Cycler® platform as described above. A molecular beacon probe was considered specific only when it
15 hybridized solely to DNA amplified from the MREJ of *S. aureus*. Molecular beacon probes found to be specific were subsequently tested for their ubiquity (i.e. ubiquitous probes detected efficiently most or all isolates of the MRSA) by hybridization to bacterial DNAs from various MRSA strains.

20 ***Bacterial strains***

The reference strains used to build proprietary *SCCmec*-chromosome right extremity junction sequence data subrepertories, as well as to test the amplification and hybridization assays, were obtained from (i) the American Type Culture
25 Collection (ATCC), (ii) the Laboratoire de santé publique du Québec (LSPQ) (Ste-Anne de Bellevue, Québec, Canada), (iii) the Centers for Disease Control and Prevention (CDC) (Atlanta, GA), (iv) the Institut Pasteur (Paris, France), and V) the Harmony Collection (London, United Kingdom) (Table 14). Clinical isolates of MRSA, MSSA, MRCNS and MSCNS from various geographical areas were also

used in this invention (Table 15). The identity of our MRSA strains was confirmed by phenotypic testing and reconfirmed by PCR analysis using *S. aureus*-specific primers and *mecA*-specific primers (SEQ ID NOs.: 69 and 81) (Martineau *et al.*, 2000, Antimicrob. Agents Chemother. **44**:231-238).

5

For sake of clarity, below is a list of the Examples, Tables, Figures and Annexes of this invention.

DESCRIPTION OF THE EXAMPLES

10

Example 1: Primers developed by Hiramatsu *et al.* can only detect MRSA strains belonging to MREP types i, ii, and iii while missing prevalent novel MREP types.

Example 2: Detection and identification of MRSA using primers specific to MREP types i, ii and iii sequences developed in the present invention.

15 **Example 3:** Development of a multiplex PCR assay on a standard thermocycler for detection and identification of MRSA based on MREP types i, ii, iii, iv and v sequences.

Example 4: Development of a real-time multiplex PCR assay on the Smart Cycler[®] for detection and identification of MRSA based on MREP types i, ii, iii, iv
20 and v sequences.

Example 5: Development of a real-time multiplex PCR assay on the Smart Cycler[®] for detection and identification of MRSA based on MREP types i, ii, iii, iv and v sequences and including an internal control.

Example 6: Detection of MRSA using the real-time multiplex assay on the Smart
25 Cycler[®] based on MREP types i, ii, iii, iv and v sequences for the detection of MRSA directly from clinical specimens.

Example 7: Development of a real-time multiplex PCR assay on the Smart Cycler[®] for detection and identification of MRSA based on MREP types i, ii, iii, iv, v, vi and vii sequences.

Example 8: Developement of real-time PCR assays on the Smart Cyclor[®] for detection and identification of MRSA based on MREP types vi, viii and ix.

DESCRIPTION OF THE TABLES

5

Table 1 provides information about all PCR primers developed by Hiramatsu *et al.* in US patent 6,156,507.

Table 2 is a compilation of results (ubiquity and specificity) for the detection of SCC*mec-orfX* right extremity junction using primers described by Hiramatsu *et al.*

10 in US patent 6,156,507 on a standard thermocycler.

Table 3 is a list of MRSA strains not amplifiable using primers targeting types I, II and III of SCC*mec-orfX* right extremity junction sequences.

Table 4 is a list of novel sequences revealed in the present invention.

Table 5 provides information about all primers developed in the present invention.

15 **Table 6** is a list of molecular beacon probes developed in the present invention.

Table 7 shows amplicon sizes of the different primer pairs described by Hiramatsu *et al.* in US patent 6,156,507 or developed in the present invention.

Table 8 provides information about primers developed in the present invention to seequence the SCC*mec*-chromosome right extremity junction.

20 **Table 9** provides information about primers developed in the present invention to obtain sequence of the complete SCC*mec*.

Table 10 is a list of the sequences available from public databases (GenBank, genome projects or US patent 6,156,507) used in the present invention to design primers and probes.

25 **Table 11** gives analytical sensitivity of the PCR assay developed in the present invention using primers targeting types I, II and III of SCC*mec-orfX* right extremity junction sequences and performed using a standard thermocycler.

Table 12 is a compilation of results (ubiquity and specificity) for the detection of MRSA using primers developed in the present invention which target types I, II

and III of *SCCmec-orfX* right extremity junction sequences and performed using a standard thermocycler.

Table 13 shows a comparison of sequence identities between the first 500 nucleotides of *SCCmec* right extremities between 9 types of MREP.

5 **Table 14** provides information about the reference strains of MRSA, MSSA, MRCNS and MSCNS used to validate the PCR assays developed in the present invention.

Table 15 provides information about the origin of clinical strains of MRSA, MSSA, MRCNS and MSCNS used to validate the PCR assays described in the
10 present invention.

Table 16 depicts the analytical sensitivity of the PCR assay developed in the present invention using primers targeting 5 types of MREP sequences and performed on a standard thermocycler.

Table 17 is a compilation of results (ubiquity and specificity) for the PCR assay
15 developed in the present invention using primers targeting 5 types of MREP sequences and performed on a standard thermocycler.

Table 18 depicts the analytical sensitivity of the PCR assay developed in the present invention using the SmartCycler[®] platform for the detection of 5 types of MREP.

20 **Table 19** is a compilation of results (ubiquity and specificity) for the PCR assay developed in the present invention using primers and a molecular beacon probe targeting 5 types of MREP sequences and performed on the SmartCycler[®] platform.

Table 20 depicts the analytical sensitivity of the PCR assay developed in the
25 present invention using the SmartCycler[®] platform for the detection of 6 MREP types.

Table 21 is a compilation of results (ubiquity and specificity) for the PCR assay developed in the present invention using primers and a molecular beacon probe

targeting 6 types of MREP sequences and performed on the Smart Cycler® platform.

DESCRIPTION OF THE FIGURES

5

Figure 1 is a diagram illustrating the position of the primers developed by Hiramatsu *et al.* (US patent 6,156,507) in the SCC*mec*-chromosome right extremity junction for detection and identification of MRSA.

Figure 2 is a diagram illustrating the position of the primers selected in the present invention in the SCC*mec-orfX* right extremity junction for detection and identification of MRSA.

Figure 3 is a diagram illustrating the position of the primers selected in the present invention to sequence new MREP types.

Figure 4 illustrates a sequence alignment of nine MREP types.

15

FIGURE LEGENDS

Figure 1. Schematic organization of types I, II and III SCC*mecorfX* right extremity junctions and localization of the primers (SEQ ID NOs: 52-63) described by Hiramatsu *et al.* for the detection and identification of MRSA. Amplicon sizes are depicted in Table 7.

Figure 2. Schematic organization of MREP types i, ii, iii, iv, v, vi, vii, viii and ix and localization of the primers and molecular beacon targeting all MREP types (SEQ ID NOs. 20, 64, 66, 67, 79, 80, 84, 112, 115, 116, 84, 163 and 164) which were developed in the present invention. Amplicon sizes are depicted in Table 7.

Figure 3. Schematic organization of the SCC*mec*-chromosome right extremity junctions and localization of the primers (SEQ IDNOs. 65, 68, 69, 70, 77, 96, 118, 126, 132, 150 and 158) developed in the present invention for the sequencing of MREP types iv, v, vi, vii, viii, ix and x.

Figure 4. Multiple sequence alignment of representatives of nine MREP types (represented by portions of SEQ IDNOs.: 1, 2, 104, 51, 50, 171, 165, 167 and 168 for types i, ii, iii, iv, v, vi, vii, viii and ix, respectively).

5 DESCRIPTION OF THE ANNEXES

The Annexes show the strategies used for the selection of primers and internal probes:

Annex I illustrates the strategy for the selection of primers from *SCCmec* and *orfX* sequences specific for *SCCmec* types I and II.

Annex II illustrates the strategy for the selection of specific molecular beacon probes for the real-time detection of *SCCmec-orfX* right extremity junctions.

As shown in these Annexes, the selected amplification primers may contain inosines and/or base ambiguities. Inosine is a nucleotide analog able to specifically bind to any of the four nucleotides A, C, G or T. Alternatively, degenerated oligonucleotides which consist of an oligonucleotide mix having two or more of the four nucleotides A, C, G or T at the site of mismatches were used. The inclusion of inosine and/or of degeneracies in the amplification primers allows mismatch tolerance thereby permitting the amplification of a wider array of target nucleotide sequences (Dieffenbach and Dveksler, 1995, PCR Primer: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Plainview, New York).

EXAMPLES

EXAMPLE 1:

Primers developed by Hiramatsu *et al.* can only detect MRSA strains belonging to MREP types i, ii, and iii while missing prevalent novel MREP types.

As shown in Figure 1, Hiramatsu *et al.* have developed various primers that can specifically hybridize to the right extremities of types I, II and III SCCmec DNAs. They combined these primers with primers specific to the *S. aureus* chromosome region located to the right of the SCCmec integration site for the detection of MRSA. The primer set (SEQ ID NOs.: 22, 24 and 28 in US patent 6,156,507 corresponding to SEQ ID NOs.: 56, 58 and 60 in the present invention) was shown by Hiramatsu *et al.* to be the most specific and ubiquitous for detection of MRSA. This set of primers gives amplification products of 1.5 kb for SCCmec type I, 1.6 kb for SCCmec type II and 1.0 kb for SCCmec type III (Table 7). The ubiquity and specificity of this multiplex PCR assay was tested on 39 MRSA strains, 41 MSSA strains, 9 MRCNS strains and 11 MSCNS strains (Table 2). One μ L of a treated standardized bacterial suspension or of a bacterial genomic DNA preparation purified from bacteria were amplified in a 20 μ L PCR reaction mixture. Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 2.5 mM MgCl₂, 0.4 μ M of each of the SCCmec- and *orfX*-specific primers (SEQ ID NOs.: 56, 58 and 60), 200 μ M of each of the four dNTPs (Pharmacia Biotech), 3.3 μ g/ μ L of BSA (Sigma), and 0.5 U *Taq* polymerase (Promega) coupled with *TaqStart*TM Antibody (BD Biosciences).

PCR reactions were then subjected to thermal cycling: 3 min at 94°C followed by 40 cycles of 60 seconds at 95°C for the denaturation step, 60 seconds at 55°C for the annealing step, and 60 seconds at 72°C for the extension step, then followed by a terminal extension of 7 minutes at 72°C using a standard thermocycler (PTC-200 from MJ Research Inc.). Detection of the PCR products was made by electrophoresis in agarose gels (2 %) containing 0.25 μ g/ml of ethidium bromide.

None of the MRCNS or MSCNS strains tested were detected with the set of primers detecting SCCmec types I, II and III. Twenty of the 39 MRSA strains tested were not detected with this multiplex PCR assay (Tables 2 and 3). One of these undetected MRSA strains corresponds to the highly epidemic MRSA Portuguese clone (strain CCRI-9504; De Lencastre *et al.*, 1994. Eur. J. Clin. Microbiol. Infect. Dis. 13:64-73) and another corresponds to the highly epidemic MRSA Canadian clone CMRSA1 (strain CCRI-9589; Simor *et al.* CCDC 1999, 25-12, June 15). These data demonstrate that the primer set developed by Hiramatsu *et al.* (SEQ ID NOs.: 22, 24 and 28 in US patent 6,156,507 corresponding to SEQ ID NOs.: 56, 58 and 60 in the present invention) is not ubiquitous for the detection of MRSA and suggest that some MRSA strains have sequences at the SCCmec right extremity junction which are different from those identified by Hiramatsu *et al.* other types of SCCmec sequences or other sequences at the right extremity of SCCmec (MREP type) are found in MRSA. A limitation of this assay is the non-specific detection of 13 MSSA strains (Table 2).

EXAMPLE 2:

Detection and identification of MRSA using primers specific to MREP types i, ii and iii sequences developed in the present invention. Based on analysis of multiple sequence alignments of *orfX* and SCCmec sequences described by Hiramatsu *et al.* or available from GenBank, a set of primers (SEQ ID NOs: 64, 66, 67) capable of amplifying short segments of types I, II and III of SCCmec-*orfX* right extremity junctions from MRSA strains and discriminating from MRCNS (Annex I and Figure 2) were designed. The chosen set of primers gives amplification products of 176 bp for SCCmec type I, 278 pb for SCCmec type II and 223 bp for SCCmec type III and allows rapid PCR amplification. These primers were used in multiplex PCR to test their ubiquity and specificity using 208 MRSA strains, 252 MSSA strains, 41 MRCNS strains and 21 MRCNS strains

(Table 12). The PCR amplification and detection was performed as described in Example 1. PCR reactions were then subjected to thermal cycling (3 minutes at 94°C followed by 30 or 40 cycles of 1 second at 95°C for the denaturation step and 30 seconds at 60°C for the annealing-extension step, and then followed by a terminal extension of 2 minutes at 72°C) using a standard thermocycler (PTC-200 from MJ Research Inc.). Detection of the PCR products was made as described in Example 1.

None of the MRCNS or MSCNS strains tested were detected with this set of primers (Table 12). However, the twenty MRSA strains which were not detected with the primer set developed by Hiramatsu *et al.* (SEQ ID NOs: 56, 58 and 60) were also not detected with the primers developed in the present invention (Tables 3 and 12). These data also demonstrate that some MRSA strains have sequences at the SCC*mec*-chromosome right extremity junction which are different from those identified by Hiramatsu *et al.* Again, as observed with the Hiramatsu primers, 13 MSSA strains were also detected non-specifically (Table 12). The clinical significance of this finding remains to be established since these apparent MSSA strains could be the result of a recent deletion in the *mec* locus (Deplano *et al.*, 2000, J. Antimicrob. Chemotherapy, **46**:617-619; Inglis *et al.*, 1990, J. Gen. Microbiol., **136**:2231-2239; Inglis *et al.*, 1993, J. Infect. Dis., **167**:323-328; Lawrence *et al.* 1996, J. Hosp. Infect., **33**:49-53; Wada *et al.*, 1991, Biochem. Biophys. Res. Comm., **176**:1319-1326).

EXAMPLE 3:

Development of a multiplex PCR assay on a standard thermocycler for detection and identification of MRSA based on MREP types i, ii, iii, iv and v sequences. Upon analysis of two of the new MREP types iv and v sequence data described in the present invention, two new primers (SEQ ID NOs.: 79 and 80)

were designed and used in multiplex with the three primers SEQ ID NOs.: 64, 66 and 67 described in Example 2. PCR amplification and detection of the PCR products was performed as described in Example 2. Sensitivity tests performed by using ten-fold or two-fold dilutions of purified genomic DNA from various MRSA strains of each MREP type showed a detection limit of 5 to 10 genome copies (Table 16). Specificity tests were performed using 0,1 ng of purified genomic DNA or 1 µl of a standardized bacterial suspension. All MRCNS or MSCNS strains tested were negative with this multiplex assay (Table 17). Twelve of the 20 MRSA strains which were not detected with the multiplex PCR described in Examples 1 and 2 were now detected with this multiplex assay. Again, as observed with the Hiramatsu primers, 13 MSSA strains were also detected non-specifically (Table 12). The eight MRSA strains (CCRI-9208, CCRI-9583, CCRI-9773, CCRI-9774, CCRI-9589, CCRI-9860, CCRI-9681, CCRI-9770) and which harbor the new MREP types vi, vii, viii, ix and x sequences described in the present invention remained undetectable.

EXAMPLE 4:

Development of a real-time multiplex PCR assay on the Smart Cycler® for detection and identification of MRSA based on MREP types i, ii, iii, iv and v sequences. The multiplex PCR assay described in Example 3 containing primers (SEQ ID NOs.: 64, 66, 67, 79 and 80) was adapted to the SmartCycler® platform (Cepheid). A molecular beacon probe specific to the *orfX* sequence was developed (SEQ ID NO. 84, see Annex II). Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 3.5 mM MgCl₂, 0.4 µM of each of the SCCmec- and *orfX*-specific primers (SEQ ID NOs.: 64, 66, 67, 79 and 80), 0.2 µM of the FAM-labeled molecular beacon probe (SEQ ID NO.: 84), 200 µM of each of the four dNTPs, 3.3 µg/µl of BSA, and 0.5 U *Taq* polymerase coupled with *TaqStart*TM Antibody. The PCR amplification on the Smart Cycler® was performed

as follows: 3 min. at 94°C for initial denaturation, then forty-five cycles of three steps consisting of 5 seconds at 95°C for the denaturation step, 15 seconds at 59°C for the annealing step and 10 seconds at 72°C for the extension step. Fluorescence detection was performed at the end of each annealing step. Sensitivity tests performed by using purified genomic DNA from several MRSA strains of each MREP type showed a detection limit of 2 to 10 genome copies (Table 18). None of the MRCNS or MSCNS were positive with this multiplex assay (Table 19). Again, as observed with the Hiramatsu primers, 13 MSSA strains were also detected non-specifically. Twelve of the twenty MRSA strains which were not detected with the multiplex PCR described in Examples 1 and 2 were detected by this multiplex assay. As described in Example 3, the eight MRSA strains which harbor the new MREP types vi, vii, viii, ix and x sequences described in the present invention remained undetectable.

EXAMPLE 5:

Development of a real-time multiplex PCR assay on the Smart Cycler® for detection and identification of MRSA based on MREP types i, ii, iii, iv and v sequences including an internal control.

The multiplex PCR assay described in Example 4 containing primers specific to MREP types i to v and *orfX* of *S. aureus* (SEQ ID NOs.: 64, 66, 67, 79 and 80) and a molecular beacon probe specific to the *orfX* sequence (SEQ ID NO. 84, see Annex II) was optimized to include an internal control to monitor PCR inhibition. This internal control contains sequences complementary to MREP type iv- and *orfX*-specific primers (SEQ ID NOs. 79 and 64). The assay also contains a TET-labeled molecular beacon probe specific to sequence within the amplicon generated by amplification of the internal control. Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 3.45 mM MgCl₂, 0.8 µM of each of the MREP-specific primers (SEQ ID NOs.: 66 and 67) and *orfX*-specific primer (SEQ ID NO.: 64), 0.4 µM of each of

the MREP-specific primers (SEQ ID NOs.: 79 and 80), 80 copies of the internal control, 0.2 μ M of the TET-labeled molecular beacon probe specific to the internal control, 0.2 μ M of the FAM-labeled molecular beacon probe (SEQ ID NO.: 84), 330 μ M of each of the four dNTPs (Pharmacia Biotech), 3.45 μ g/ μ l of BSA (Sigma), and 0.875 U *Taq* polymerase (Promega) coupled with *TaqStart*TM Antibody (BD Biosciences). The PCR amplification on the Smart Cycler[®] was performed as follows: 3 min. at 95°C for initial denaturation, then forty-eight cycles of three steps consisting of 5 seconds at 95°C for the denaturation step, 15 seconds at 60°C for the annealing step and 15 seconds at 72°C for the extension step. Sensitivity tests performed by using purified genomic DNA from one MRSA strain of each MREP type (i to v) showed a detection limit of 2 to 10 genome copies. None of the 26 MRCNS or 10 MSCNS were positive with this multiplex assay. Again, as observed with the Hiramatsu primers, 13 MSSA strains were also detected non-specifically. As described in Examples 3 and 4, the eight MRSA strains which harbor the new MREP types vi to x sequences described in the present invention remained undetectable.

EXAMPLE 6:

Detection of MRSA using the real-time multiplex assay on the Smart Cycler[®] based on MREP types i, ii, iii, iv and v sequences directly from clinical specimens. The assay described in Example 5 was adapted for detection directly from clinical specimens. A total of 142 nasal swabs collected during a MRSA hospital surveillance program at the Montreal General Hospital (Montreal, Quebec, Canada) were tested. The swab samples were tested at the Centre de Recherche en Infectiologie de l'Université Laval within 24 hours of collection. Upon receipt, the swabs were plated onto mannitol agar and then the nasal material from the same swab was prepared with a simple and rapid specimen preparation protocol

described in co-pending patent application number US 60/306,163. Classical identification of MRSA was performed by standard culture methods.

The PCR assay described in Example 5 detected 33 of the 34 samples positive for MRSA based on the culture method. As compared to culture, the PCR assay detected 8 additional MRSA positive specimens for a sensitivity of 97.1 % and a specificity of 92.6 %. This multiplex PCR assay represents a rapid and powerful method for the specific detection of MRSA carriers directly from nasal specimens and can be used with any type of clinical specimens such as wounds, blood or blood culture, CSF, etc.

EXAMPLE 7:

Development of a real-time multiplex PCR assay on the Smart Cycler® for detection and identification of MRSA based on MREP types i, ii, iii, iv, v and vii sequences. Upon analysis of the new MREP type vii sequence data described in the present invention (SEQ ID NOs.: 165 and 166), two new primers (SEQ ID NOs.: 112 and 113) were designed and tested in multiplex with the three primers SEQ ID NOs.: 64, 66 and 67 described in Example 2. Primer SEQ ID NO.: 112 was selected for use in the multiplex based on its sensitivity. Three molecular beacon probes specific to the *orfX* sequence which allowed detection of two sequence polymorphisms identified in this region of the *orfX* sequence, based on analysis of SEQ ID NOs.: 173-186, were also used in the multiplex (SEQ ID NOs.: 84, 163 and 164). Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 3.45 mM MgCl₂, 0.8 µM of each of the SCC*mec*-specific primers (SEQ ID NOs.: 66 and 67) and *orfX*-specific primer (SEQ ID NO.: 64), 0.4 µM of each of the SCC*mec*-specific primers (SEQ ID NOs.: 79 and 80), 0.2 µM of the FAM-labeled molecular beacon probe (SEQ ID NO.: 84), 330 µM of each of the four dNTPs (Pharmacia Biotech), 3.45 µg/µl of BSA (Sigma), and 0.875 U of

Taq polymerase (Promega) coupled with *TaqStart*TM Antibody (BD Biosciences). The PCR amplification on the Smart Cycler[®] was performed as follows: 3 min. at 95°C for initial denaturation, then forty-eight cycles of three steps consisting of 5 seconds at 95°C for the denaturation step, 15 seconds at 60°C for the annealing step and 15 seconds at 72°C for the extension step. The detection of fluorescence was done at the end of each annealing step. Sensitivity tests performed by using purified genomic DNA from several MRSA strains of each MREP type showed a detection limit of 2 genome copies (Table 20). None of the 26 MRCNS or 8 MSCNS were positive with this multiplex assay. Again, as observed with the Hiramatsu primers, 13 MSSA strains were also detected non-specifically (Table 21). Four of the strains which were not detected with the multiplex assay for the detection of MREP types i to v were now detected with this multiplex assay while the four MRSA strains (CCRI-9208, CCRI-9770, CCRI-9681, CCRI-9860) which harbor the MREP types vi, viii, ix and x described in the present invention remained undetectable.

EXAMPLE 8:

Developement of real-time PCR assays on the Smart Cycler[®] for detection and identification of MRSA based on MREP types vi, viii, ix. Upon analysis of the new MREP types vi, viii and ix sequence data described in the present invention, one new primers specific to MREP type vi (SEQ ID NO.: 201), one primer specific to MREP type viii (SEQ ID NO.: 115), a primer specific to MREP type ix (SEQ ID NO.: 109) and a primer specific to both MREP types viii and ix (SEQ ID NO.: 116) were designed. Each PCR primer was used in combination with the *orfX*-specific primer (SEQ ID NO.: 64) and tested against its specific target strain. Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 3.45 mM MgCl₂, 0.4 μM of each of the SCC*mec*- and *orfX*-specific primers, 200 μM of each of the four dNTPs, 3.4 μg/μl of BSA, and 0.875

U *Taq* polymerase coupled with *TaqStart*TM Antibody. The PCR amplification was performed as described in Example 7. Sensitivity tests performed by using genomic DNA purified from their respective MRSA target strains showed that the best primer pair combination was SEQ ID NOs.: 64 and 115 for the detection of MREP types viii and ix simultaneously. These new *SCCmec*-specific primers may be used in multiplex with primers specific to MREP types i, ii, iii, iv, v and vii (SEQ ID NOs.: 64, 66, 67, 79 and 80) described in previous examples to provide a more ubiquitous MRSA assay.

In conclusion, we have improved the ubiquity of detection of MRSA strains. New MREJ types iv to x have been identified. Amongst strains representative of these new types, Hiramitsu's primers and/or probes succeeded in detecting less than 50% thereof. We have therefore amply passed the bar of at least 50% ubiquity, since our primers and probes were designed to detect 100% of the strains tested as representatives of MREJ types iv to ix. Therefore, although ubiquity depends on the pool of strains and representatives that are underanalyse, we know now that close to 100% ubiquity is an attainable goal, when using the sequences of the right junctions (MREJ) to derive probes and primers dealing with polymorphism in this region. Depending on how many unknown types of MREJ exist, we have a margin of manoeuvre going from 50% (higher than Hiramitsu's primers for the tested strains) to 100% if we sequence all the existing MREJs to derive properly the present diagnostic tools and methods, following the above teachings.

This invention has been described herein above, and it is readily apparent that modifications can be made thereto without departing from the spirit of this invention. These modifications are under the scope of this invention, as defined in the appended claims.

Table 1. PCR amplification primers reported by Hiramatsu et al. in US patent 6,156,507 found in the sequence listing

5	SEQ ID NO.:	Target	Position ^{a,b}	SEQ ID NO.:
	(present invention)			(US pat. 6,156,507)
10	52	MREP types i and ii	480	18
	53	MREP types i and ii	758	19
	54	MREP types i and ii	927	20
	55	MREP types i and ii	1154	21
	56	MREP types i and ii	1755	22
15	57	MREP types i and ii	2302	23
	58	MREP type iii	295 ^c	24
	59	<i>orfX</i>	1664	25
	60	<i>orfSA0022</i> ^d	3267	28
	61	<i>orfSA0022</i> ^d	3585	27
20	62	<i>orfX</i>	1389	26
	63	<i>orfSA0022</i> ^d	2957	29

^a Position refers to nucleotide position of the 5' end of primer.

^b Numbering for SEQ ID NOs.: 52-57 refers to SEQ ID NO.: 2; numbering for SEQ ID NO.: 58 refers to SEQ ID NO.: 4; numbering for SEQ ID NOs.: 59-63 refers to SEQ ID NO.: 3.

^c Primer is reverse-complement of target sequence.

^d *orfSA0022* refers to the open reading frame designation from GenBank accession number AP003129 (SEQ ID NO.: 231).

Table 2. Specificity and ubiquity tests performed on a standard thermocycler using the optimal set of primers described by Hiramatsu et al. (SEQ ID NOs. : 22, 24 and 28 in US patent 6,156,507 corresponding to SEQ ID NOs.: 56, 58 and 60, respectively, in the present invention) for the detection of MRSA

Strains	PCR results for SCCmec - <i>orfX</i> right extremity junction	
	Positive (%)	Negative (%)
MRSA - 39 strains	19 (48.7)	20 (51.2)
MSSA - 41 strains	13 (31.7)	28 (68.3)
MRCNS - 9 strains*	0 (0%)	9 (100%)
MSCNS - 11 strains*	0 (0%)	11 (100%)

* Details regarding CNS strains:

MRCNS : *S. caprae* (1)
S. cohnii cohnii (1)
S. epidermidis (1)
S. haemolyticus (2)
S. hominis (1)
S. sciuri (1)
S. simulans (1)
S. warneri (1)

MSCNS : *S. cohnii cohnii* (1)
S. epidermidis (1)
S. equorum (1)
S. gallinarum (1)
S. haemolyticus (1)
S. lentus (1)
S. lugdunensis (1)
S. saccharolyticus (1)
S. saprophyticus (2)
S. xylosus (1)

Table 3. Origin of MRSA strains not amplifiable using primers developed by Hiramatsu et al. (SEQ ID NOs.: 22, 24 and 28 in US patent 6,156,507 corresponding to SEQ ID NOs.: 56, 58 and 60, respectively, in the present invention) as well as primers developed in the present invention targeting MREP types i, ii and iii (SEQ ID NOs.: 64, 66 and 67)

<i>Staphylococcus aureus</i> strain designation:		Origin
Original	CCRI ^a	
ATCC BAA-40 ^b	CCRI-9504	Portugal
ATCC 33592	CCRI-178	USA
R991282	CCRI-2025	Québec, Canada
4508	CCRI-9208	Québec, Canada
19121	CCRI-8895	Denmark
Z109	CCRI-8903	Denmark
45302	CCRI-1263	Ontario, Canada
R655	CCRI-1324	Québec, Canada
MA 50428	CCRI-1311	Québec, Canada
MA 50609	CCRI-1312	Québec, Canada
MA 51363	CCRI-1331	Québec, Canada
MA 51561	CCRI-1325	Québec, Canada
14A0116	CCRI-9681	Poland
23 (CCUG 41787)	CCRI-9860	Sweden
SE26-1	CCRI-9770	Ontario, Canada
SE1-1	CCRI-9583	Ontario, Canada
ID-61880 ^c	CCRI-9589	Ontario, Canada
SE47-1	CCRI-9773	Ontario, Canada
SE49-1	CCRI-9774	Ontario, Canada
39795-2	CCRI-1377	Québec, Canada

^a CCRI stands for "Collection of the Centre de Recherche en Infectiologie".

^b Portuguese clone.

^c Canadian clone EMRSA1.

Table 4. *Staphylococcus aureus* MREJ nucleotide sequences revealed in the present invention

5	SEQ ID NO.	<i>Staphylococcus aureus</i> strain designation:		Genetic Target
		Original	CCRI ^a	
10	27	R991282	CCRI-2025	<i>mecA</i>
	28	45302	CCRI-1263	<i>mecA</i>
	29	MA 50428	CCRI-1311	<i>mecA</i>
	30	MA 51363	CCRI-1331	<i>mecA</i>
	31	39795-2	CCRI-1377	<i>mecA</i> and 1.5 kb of downstream region
15	42	ATCC 33592	CCRI-178	MREP type iv
	43	19121	CCRI-8895	MREP type iv
	44	Z109	CCRI-8903	MREP type iv
	45	R655	CCRI-1324	MREP type iv
	46	MA 51363	CCRI-1331	MREP type iv
20	47	45302	CCRI-1263	MREP type v
	48	39795-2	CCRI-1377	MREP type v
	49	MA 50428	CCRI-1311	MREP type v
	50	R991282	CCRI-2025	MREP type v
	51	ATCC BAA-40	CCRI-9504	MREP type iv
25	165	SE1-1	CCRI-9583	MREP type vii
	166	ID-61880	CCRI-9589	MREP type vii
	167	23 (CCUG 41787)	CCRI-9860	MREP type viii
	168	14A016	CCRI-9681	MREP type ix
	171	4508	CCRI-9208	MREP type vi
30	172	SE26-1	CCRI-9770	<i>orfSA0021^b</i> and 75 bp of <i>orfSA0022^b</i>
	173	26 (98/10618)	CCRI-9864	MREP type ii
	174	27 (98/26821)	CCRI-9865	MREP type ii
	175	28 (24344)	CCRI-9866	MREP type ii
	176	12 (62305)	CCRI-9867	MREP type ii
35	177	22 (90/14719)	CCRI-9868	MREP type ii
	178	23 (98/14719)	CCRI-9869	MREP type ii
	179	32 (97S99)	CCRI-9871	MREP type ii
	180	33 (97S100)	CCRI-9872	MREP type ii
	181	38 (825/96)	CCRI-9873	MREP type ii
40	182	39 (842/96)	CCRI-9874	MREP type ii
	183	43 (N8-892/99)	CCRI-9875	MREP type ii
	184	46 (9805-0137)	CCRI-9876	MREP type iii
	185	1	CCRI-9882	MREP type ii
	186	29	CCRI-9885	MREP type ii
45	189	SE1-1	CCRI-9583	<i>mecA</i> and 2.2 kb of downstream region, including IS431 <i>mec</i>
	190	ATCC BAA-40	CCRI-9504	<i>mecA</i> and 1.5 kb of downstream region
	191	4508	CCRI-9208	<i>mecA</i> and 0.9 kb of downstream region
	192	ID-61880	CCRI-9589	<i>mecA</i> and 0.9 kb of downstream region
	193	14A016	CCRI-9681	<i>mecA</i> and 0.9 kb of downstream region
50	195	SE26-1	CCRI-9770	<i>mecA</i> and 1.5 kb of downstream region, including IS431 <i>mec</i>
	197	ATCC 43300	CCRI-175	MREP type ii
	198	R522	CCRI-1262	MREP type iii
	199	13370	CCRI-8894	MREP type i
	219	ATCC BAA-40	CCRI-9504	<i>tetK</i>

Table 4. *Staphylococcus aureus* MREJ nucleotide sequences revealed in the present invention (continued)

5	SEQ ID NO.	<i>Staphylococcus aureus</i> strain designation:		Genetic Target ^a
		Original	CCRI ^b	
10	220	MA 51363	CCRI-1331	<i>mecA</i> and 1.5 kb of downstream region
	221	39795-2	CCRI-1377	IS431 <i>mec</i> and 0.6 kb of upstream region
	222	R991282	CCRI-2025	<i>mecA</i> and 1.5 kb of downstream region
	223	R991282	CCRI-2025	IS431 <i>mec</i> and 0.6 kb of upstream region
	224	23 (CCUG 41787)	CCRI-9860	<i>mecA</i> and 1.5 kb of downstream region
	225	23 (CCUG 41787)	CCRI-9860	IS431 <i>mec</i> and 0.6 kb of upstream region
	233	14A016	CCRI-9681	MREP type ix

^a CCRI stands for "Collection of the Centre de Recherche en Infectiologie".

^b *orfSA0021* and *orfSA0022* refer to the open reading frame designation from GenBank accession number AF003129 (SEQ ID NO.: 231).

Table 5. PCR primers developed in the present invention

	SEQ ID NO.	Target	Originating DNA	
			Position ^a	SEQ ID NO.
5	64	<i>orfX</i>	1720	3
	70	<i>orfX</i>	1796	3
	71	<i>orfX</i>	1712	3
	72	<i>orfX</i>	1749	3
10	73	<i>orfX</i>	1758	3
	74	<i>orfX</i>	1794	3
	75	<i>orfX</i>	1797	3
	76	<i>orfX</i>	1798	3
15	66	MREP types i and ii	2327	2
	100	MREP types i and ii	2323	2
	101	MREP types i and ii	2314	2
	97	MREP type ii	2434	2
20	99	MREP type ii	2434	2
	67	MREP type iii	207 ^b	4
	98	MREP type iii	147 ^b	4
	102	MREP type iii	251 ^b	4
25	79	MREP type iv	74 ^b	43
	80	MREP type v	50 ^b	47
	109	MREP type ix	652 ^b	168
	204	MREP type vi	642 ^b	171
30	112	MREP type vii	503 ^b	165
	113	MREP type vii	551 ^b	165
	115	MREP type viii	514 ^b	167
	116	MREP type viii	601 ^b	167

^a Position refers to nucleotide position of 5' end of primer.

^b Primer is reverse-complement of target sequence.

Table 6. Molecular beacon probes developed in the present invention

	SEQ ID NO.	Target	Position
5	32	<i>orfX</i>	86 ^a
	83	<i>orfX</i>	86 ^a
	84	<i>orfX</i>	34 ^{a,b}
	160	<i>orfX</i>	55 ^{a,b}
10	161	<i>orfX</i>	34 ^{a,b}
	162	<i>orfX</i>	114 ^a
	163	<i>orfX</i>	34 ^{a,b}
	164	<i>orfX</i>	34 ^{a,b}
15			

^a Position refers to nucleotide position of the 5' end of the molecular beacon's loop on SEQ ID NO.: 3.

^b Sequence of molecular beacon's loop is reverse-complement of SEQ ID NO.: 3.

Table 7. Length of amplicons obtained with the different primer pairs which are objects of the present invention

SEQ ID NO.	Target ^d	Amplicon length ^a
5	59/52 ^b <i>orfX</i> /MREP type i and ii	2079 (type i);2181 (type ii)
	59/53 ^b <i>orfX</i> /MREP type i and ii	1801 (type i);1903 (type ii)
	59/54 ^b <i>orfX</i> /MREP type i and ii	1632 (type i);1734 (type ii)
	59/55 ^b <i>orfX</i> /MREP type i and ii	1405 (type i);1507 (type ii)
10	59/56 ^b <i>orfX</i> /MREP type i and ii	804 (type i);906 (type ii)
	59/57 ^b <i>orfX</i> /MREP type i and ii	257 (type i);359 (type ii)
	60/52 ^b <i>orfSA0022</i> /MREP type i and ii	2794 (type i);2896 (type ii)
	60/53 ^b <i>orfSA0022</i> /MREP type i and ii	2516 (type i);2618 (type ii)
	60/54 ^b <i>orfSA0022</i> /MREP type i and ii	2347 (type i);2449 (type ii)
15	60/55 ^b <i>orfSA0022</i> /MREP type i and ii	2120 (type i);2222 (type ii)
	60/56 ^b <i>orfSA0022</i> /MREP type i and ii	1519 (type i);1621 (type ii)
	60/57 ^b <i>orfSA0022</i> /MREP type i and ii	972 (type i);1074 (type ii)
	61/52 ^b <i>orfSA0022</i> /MREP type i and ii	2476 (type i);2578 (type ii)
	61/53 ^b <i>orfSA0022</i> /MREP type i and ii	2198 (type i);2300 (type ii)
20	61/54 ^b <i>orfSA0022</i> /MREP type i and ii	2029 (type i);2131 (type ii)
	61/55 ^b <i>orfSA0022</i> /MREP type i and ii	1802 (type i);1904 (type ii)
	61/56 ^b <i>orfSA0022</i> /MREP type i and ii	1201 (type i);1303 (type ii)
	61/57 ^b <i>orfSA0022</i> /MREP type i and ii	654 (type i);756 (type ii)
	62/52 ^b <i>orfX</i> /MREP type i and ii	2354 (type i);2456 (type ii)
25	62/53 ^b <i>orfX</i> /MREP type i and ii	2076 (type i);2178 (type ii)
	62/54 ^b <i>orfX</i> /MREP type i and ii	1907 (type i);2009 (type ii)
	62/55 ^b <i>orfX</i> /MREP type i and ii	1680 (type i);1782 (type ii)
	62/56 ^b <i>orfX</i> /MREP type i and ii	1079 (type i);1181 (type ii)
	62/57 ^b <i>orfX</i> /MREP type i and ii	532 (type i);634 (type ii)
30	63/52 ^b <i>orfSA0022</i> /MREP type i and ii	3104 (type i);3206 (type ii)
	63/53 ^b <i>orfSA0022</i> /MREP type i and ii	2826 (type i);2928 (type ii)
	63/54 ^b <i>orfSA0022</i> /MREP type i and ii	2657 (type i);2759 (type ii)
	63/55 ^b <i>orfSA0022</i> /MREP type i and ii	2430 (type i);2532 (type ii)
	63/56 ^b <i>orfSA0022</i> /MREP type i and ii	1829 (type i);1931 (type ii)
35	63/57 ^b <i>orfSA0022</i> /MREP type i and ii	1282 (type i);1384 (type ii)
	59/58 ^b <i>orfX</i> /MREP type iii	361
	60/58 ^b <i>orfSA0022</i> /MREP type iii	1076
	61/58 ^b <i>orfSA0022</i> /MREP type iii	758
	62/58 ^b <i>orfX</i> /MREP type iii	656
40	63/58 ^b <i>orfSA0022</i> /MREP type iii	1386
	70/66 <i>orfX</i> /MREP type i and ii	100 (type i);202 (type ii)
	70/67 <i>orfX</i> /MREP type iii	147 (type iii)
	64/66 ^c <i>orfX</i> /MREP type i and ii	176 (type i);278 (type ii)
	64/67 ^c <i>orfX</i> /MREP type iii	223
45	64/79 ^c <i>orfX</i> /MREP type iv	215
	64/80 ^c <i>orfX</i> /MREP type v	196
	64/97 ^c <i>orfX</i> /MREP type ii	171
	64/98 ^c <i>orfX</i> /MREP type iii	163
	64/99 ^c <i>orfX</i> /MREP type ii	171
50	64/100 ^c <i>orfX</i> /MREP types i and ii	180 (type i);282 (type ii)
	64/101 ^c <i>orfX</i> /MREP types i and ii	189 (type i);291 (type ii)
	64/102 ^c <i>orfX</i> /MREP type iii	263
	64/109 ^c <i>orfX</i> /MREP type ix	369
	64/204 ^c <i>orfX</i> /MREP type vi	348
55	64/112 ^c <i>orfX</i> /MREP type vii	214
	64/113 ^c <i>orfX</i> /MREP type vii	263
	64/115 ^c <i>orfX</i> /MREP type viii	227
	64/116 ^c <i>orfX</i> /MREP type viii	318

^a Amplicon length is given in base pairs for MREP types amplified by the set of primers.

^b Set of primers described by Hiramatsu et al. in US patent 6,156,507.

^c Set of primers developed in the present invention.

^d *orfSA0022* refers to the open reading frame designation from GenBank accession number AP003129 (SEQ ID NO.: 231).

Table 8. Other primers developed in the present invention

	SEQ ID NO.	Target	Originating DNA	
			Position ^a	SEQ ID NO.
5	77	MREP type iv	993	43
	65	MREP type v	636	47
	70	<i>orfX</i>	1796	3
	68	<i>IS431</i>	626	92
10	69	<i>mecA</i>	1059	78
	96	<i>mecA</i>	1949	78
	81	<i>mecA</i>	1206	78
	114	MREP type vii	629 ^b	165
	117	MREP type ii	856	194
15	118	MREP type ii	974 ^b	194
	119	MREP type vii	404	189
	120	MREP type vii	477 ^b	189
	123	MREP type vii	551	165
	124	MREP type ii	584	170
20	125	MREP type ii	689 ^b	170
	126	<i>orfSA0021</i>	336	231
	127	<i>orfSA0021</i>	563	231
	128	<i>orfSA0022^d</i>	2993	231
	129	<i>orfSA0022^d</i>	3467 ^b	231
25	132	<i>orfX</i>	3700	231
	145	MREP type iv	988	51
	146	MREP type v	1386	51
	147	MREP type iv	891 ^b	51
	148	MREP type ix	664	168
30	149	MREP type ix	849 ^b	168
	150	MREP type vii	1117 ^b	165
	151	MREP type vii	1473	189
	152	<i>IS431mec</i>	1592 ^b	189
	154	MREP type v	996 ^b	50
35	155	MREP type v	935	50
	156	<i>tetK</i> from plasmid pT181	1169 ^b	228
	157	<i>tetK</i> from plasmid pT181	136	228
	158	<i>orfX</i>	2714 ^b	2
	159	<i>orfX</i>	2539	2
40	187	MREP type viii	967 ^b	167
	188	MREP type viii	851	167

^a Position refers to nucleotide position of the 5' end of primer.

45 ^b Primer is reverse-complement of target sequence.

Table 9. Amplification and/or sequencing primers developed in the present invention

5	SEQ ID NO.	Target	Originating DNA	
			Position ^a	SEQ ID NO.
	85	<i>S. aureus</i> chromosome	197 ^b	35
	86	<i>S. aureus</i> chromosome	198 ^b	37
	87	<i>S. aureus</i> chromosome	197 ^b	38
10	88	<i>S. aureus</i> chromosome	1265 ^b	39
	89	<i>S. aureus</i> chromosome	1892	3
	103	<i>orfX</i>	1386	3
	105	MREP type i	2335	2
	106	MREP type ii	2437	2
15	107	MREP type iii	153 ^b	4
	108	MREP type iii	153 ^b	4
	121	MREP type vii	1150	165
	122	MREP type vii	1241 ^b	165
	130	<i>orfX</i>	4029 ^b	231
20	131	region between <i>orfSA0022</i> and <i>orfSA0023</i> ^d	3588	231
	133	<i>merB</i> from plasmid pI258	262	226
	134	<i>merB</i> from plasmid pI258	539 ^b	226
	135	<i>merR</i> from plasmid pI258	564	226
	136	<i>merR</i> from plasmid pI258	444	227
25	137	<i>merR</i> from plasmid pI258	529	227
	138	<i>merR</i> from plasmid pI258	530 ^b	227
	139	<i>rep</i> from plasmid pUB110	796	230
	140	<i>rep</i> from plasmid pUB110	761 ^b	230
	141	<i>rep</i> from plasmid pUB110	600	230
30	142	<i>aadD</i> from plasmid pUB110	1320 ^b	229
	143	<i>aadD</i> from plasmid pUB110	759	229
	144	<i>aadD</i> from plasmid pUB110	646	229
	153	MREP type vii	1030	165
	200	<i>orfSA0022</i> ^d	871 ^c	231
35	201	<i>orfSA0022</i> ^d	1006	231
	202	MREP type vi	648	171
	203	MREP type vi	883 ^b	171
	205	MREP type ix	1180	168
	206	MREP type ix	1311 ^b	233
40	207	MREP type viii	1337	167
	208	MREP type viii	1441 ^b	167
	209	<i>ccrA</i>	184	232
	210	<i>ccrA</i>	385	232
	211	<i>ccrA</i>	643 ^b	232
45	212	<i>ccrA</i>	1282 ^b	232
	213	<i>ccrB</i>	1388	232
	214	<i>ccrB</i>	1601	232
	215	<i>ccrB</i>	2139 ^b	232
	216	<i>ccrB</i>	2199 ^b	232
50	217	<i>ccrB</i>	2847 ^b	232
	218	<i>ccrB</i>	2946 ^b	232

^a Position refers to nucleotide position of the 5' end of primer.

^b Primer is reverse-complement of target sequence.

55 ^c Primer contains two mismatches.

^d *orfSA0022* and *orfSA0023* refer to the open reading frame designation from GenBank accession number AP003129 (SEQ ID NO.: 231).

Table 10. Origin of the nucleic acids and/or sequences available from public databases found in the sequence listing

SEQ ID NO.	Staphylococcal strain	Source	Accession number	Genetic Target ^{a, b}
5				
1	NCTC 10442	Database	AB033763	SCCmec type I MREJ
2	N315	Database	D86934	SCCmec type II MREJ
3	NCTC 8325	Database	AB014440	MSSA chromosome
10	86/560	Database	AB013471	SCCmec type III MREJ
4	86/961	Database	AB013472	SCCmec type III MREJ
5	85/3907	Database	AB013473	SCCmec type III MREJ
6	86/2652	Database	AB013474	SCCmec type III MREJ
7	86/1340	Database	AB013475	SCCmec type III MREJ
8	86/1762	Database	AB013476	SCCmec type III MREJ
15	86/2082	Database	AB013477	SCCmec type III MREJ
9	85/2111	Database	AB013478	SCCmec type III MREJ
10	85/5495	Database	AB013479	SCCmec type III MREJ
11	85/1836	Database	AB013480	SCCmec type III MREJ
12	85/2147	Database	AB013481	SCCmec type III MREJ
13	85/3619	Database	AB013482	SCCmec type III MREJ
14	85/3566	Database	AB013483	SCCmec type III MREJ
15	85/2232	Database	AB014402	SCCmec type II MREJ
16	85/2235	Database	AB014403	SCCmec type II MREJ
25	MR108	Database	AB014404	SCCmec type II MREJ
17	85/9302	Database	AB014430	SCCmec type I MREJ
18	85/9580	Database	AB014431	SCCmec type I MREJ
19	85/1940	Database	AB014432	SCCmec type I MREJ
20	85/6219	Database	AB014433	SCCmec type I MREJ
21	64/4176	Database	AB014434	SCCmec type I MREJ
22	64/3846	Database	AB014435	SCCmec type I MREJ
23	HUC19	Database	AF181950	SCCmec type II MREJ
24	G3	US 6,156,507	SEQ ID NO.: 15	<i>S. epidermidis</i>
25				SCCmec type II MREJ
35	34	US 6,156,507	SEQ ID NO.: 16	<i>S. haemolyticus</i>
36				SCCmec type II MREJ
37	35	US 6,156,507	SEQ ID NO.: 9	<i>S. aureus</i> chromosome
38	36	US 6,156,507	SEQ ID NO.: 10	<i>S. aureus</i> chromosome
39	37	US 6,156,507	SEQ ID NO.: 12	<i>S. aureus</i> chromosome
40	38	US 6,156,507	SEQ ID NO.: 13	<i>S. aureus</i> chromosome
41	39	Genome project ^c		<i>S. aureus</i> chromosome
42	40	Genome project ^c		SCCmec type II MREJ
43	41	Genome project ^d		SCCmec type I MREJ
44	78	NCTC 8325	X52593	<i>mecA</i>
45	82	NCTC 10442	AB033763	<i>mecA</i>
46	90	N315	D86934	<i>mecA</i>
47	91	85/2082	AB037671	<i>mecA</i>
48	92	NCTC 10442	AB033763	IS431
49	93	N315	D86934	IS431
50	94	HUC19	AF181950	IS431
51	95	NCTC 8325	X53818	IS431
52	104	85/2082	AB037671	SCCmec type III MREJ
53	226	unknown	L29436	<i>merB</i> on plasmid pI258
54	227	unknown	L29436	<i>merR</i> on plasmid pI258
55	228	unknown	S67449	<i>tetK</i> on plasmid pT181
56	229	HUC19	AF181950	<i>aadD</i> on plasmid pUB110
57	230	HUC19	AF181950	<i>rep</i> on plasmid pUB110
58	231	N315	AP003129	<i>orfSA0021</i> , <i>orfSA0022</i> , <i>orfSA0023</i>
60	232	85/2082	AB037671	<i>ccrA/ccrB</i>

^a MREJ refers to *mec* right extremity junction and includes sequences from SCCmec-right extremity and chromosomal DNA to the right of SCCmec integration site.

^b Unless otherwise specified, all sequences were obtained from *S. aureus* strains.

^c Sanger Institute genome project (<http://www.sanger.ac.uk>).

^d TIGR genome project (<http://www.tigr.org>).

Table 11. Analytical sensitivity of the MRSA-specific PCR assay targeting MREP types i, ii and iii on a standard thermocycler using the set of primers developed in the present invention (SEQ ID NOs.: 64, 66 and 67)

5

Strain designation :		Detection limit
Original	CCRI ^a (MREP type)	(number of genome copies)
13370	CCRI-8894 (I)	5
ATCC 43300	CCRI-175 (II)	2
35290	CCRI-1262 (III)	2

^a CCRI stands for "Collection of the Centre de Recherche en Infectiologie".

Table 12. Specificity and ubiquity tests performed on a standard thermocycler using the set of primers targeting MREP types i, ii and iii developed in the present invention (SEQ ID NOs.: 64, 66 and 67) for the detection of MRSA

5

Strains	PCR results for MREJ	
	Positive (%)	Negative (%)
MRSA - 208 strains	188 (90.4)	20 (9.6)
MSSA - 252 strains	13 (5.2)	239 (94.8)
MRCNS - 41 strains*	0	42 (100)
MSCNS - 21 strains*	0	21 (100)

* Details regarding CNS strains:

10	MRCNS :	<i>S. caprae</i> (2)
		<i>S. cohnii cohnii</i> (3)
		<i>S. cohnii urealyticum</i> (4)
		<i>S. epidermidis</i> (8)
		<i>S. haemolyticus</i> (9)
15		<i>S. hominis</i> (4)
		<i>S. sciuri</i> (4)
		<i>S. sciuri sciuri</i> (1)
		<i>S. simulans</i> (3)
		<i>S. warneri</i> (3)
20	MSCNS :	<i>S. cohnii cohnii</i> (1)
		<i>S. epidermidis</i> (3)
		<i>S. equorum</i> (2)
		<i>S. felis</i> (1)
25		<i>S. gallinarum</i> (1)
		<i>S. haemolyticus</i> (1)
		<i>S. hominis</i> (1)
		<i>S. lentus</i> (1)
		<i>S. lugdunensis</i> (1)
30		<i>S. saccharolyticus</i> (1)
		<i>S. saprophyticus</i> (5)
		<i>S. simulans</i> (1)
		<i>S. warneri</i> (1)
		<i>S. xylosus</i> (1)

Table 13. Percentage of sequence identity for the first 500 nucleotides of SCCmec right extremities between all 9 types of MREP^{a,b}

MREP type	i	ii	iii	iv	v	vi	vii	viii	ix
i	--	79.2	42.8	42.8	41.2	44.4	44.6	42.3	42.1
ii			43.9	47.5	44.7	41.7	45.0	52.0	57.1
iii				46.8	44.5	42.9	45.0	42.8	45.2
iv					45.8	41.4	44.3	48.0	41.3
v						45.4	43.7	47.5	44.3
vi							45.1	41.1	47.2
vii								42.8	40.9
viii									55.2
ix									--

5

^a "First 500 nucleotides" refers to the 500 nucleotides within the SCCmec right extremity, starting from the integration site of SCCmec in the *Staphylococcus aureus* chromosome as shown on Figure 4.

10 ^b Sequences were extracted from SEQ ID NOs.: 1, 2, 104, 51, 50, 171, 165, 167, and 168 for types i to ix, respectively.

Table 14. Reference strains used to test sensitivity and/or specificity and/or ubiquity of the MRSA-specific PCR assays targeting MREJ sequences

Staphylococcal species	Strains	Source ^a
MRSA (n = 45)	33591	ATCC
	33592	ATCC
	33593	ATCC
	BAA-38	ATCC
	BAA-39	ATCC
	BAA-40	ATCC
	BAA-41	ATCC
	BAA-42	ATCC
	BAA-43	ATCC
	BAA-44	ATCC
	F182	CDC
	23 (CCUG 41787)	HARMONY Collection
	ID-61880 (EMRSA1)	LSPQ
	MA 8628	LSPQ
	MA 50558	LSPQ
	MA 50428	LSPQ
	MA 50609	LSPQ
	MA 50884	LSPQ
	MA 50892	LSPQ
	MA 50934	LSPQ
	MA 51015	LSPQ
	MA 51056	LSPQ
	MA 51085	LSPQ
	MA 51172	LSPQ
	MA 51222	LSPQ
	MA 51363	LSPQ
	MA 51561	LSPQ
	MA 52034	LSPQ
	MA 52306	LSPQ
	MA 51520	LSPQ
	MA 51363	LSPQ
	98/10618	HARMONY Collection
	98/26821	HARMONY Collection
	24344	HARMONY Collection
	62305	HARMONY Collection
	90/10685	HARMONY Collection
	98/14719	HARMONY Collection
	97S99	HARMONY Collection
	97S100	HARMONY Collection
	825/96	HARMONY Collection
	842/96	HARMONY Collection
	N8-890/99	HARMONY Collection
	9805-01937	HARMONY Collection
	1	Kreiswirth-1
	29	Kreiswirth-1
MRCNS (n = 4)	29060	ATCC
	35983	ATCC
	35984	ATCC
	2514	LSPQ

Table 14. Reference strains used to test sensitivity and/or specificity and/or ubiquity of the MRSA-specific PCR assays targeting MREJ sequences(continued)

Staphylococcal species	Strains	Source
MSSA (n = 28)	MA 52263	LSPQ
	6538	ATCC
	13301	ATCC
	25923	ATCC
	27660	ATCC
	29213	ATCC
	29247	ATCC
	29737	ATCC
	RN 11	CDC
	RN 3944	CDC
	RN 2442	CDC
	7605060113	CDC
	BM 4611	Institut Pasteur
	BM 3093	Institut Pasteur
	3511	LSPQ
	MA 5091	LSPQ
	MA 8849	LSPQ
	MA 8871	LSPQ
	MA 50607	LSPQ
	MA 50612	LSPQ
	MA 50848	LSPQ
	MA 51237	LSPQ
	MA 51351	LSPQ
	MA 52303	LSPQ
	MA 51828	LSPQ
	MA 51891	LSPQ
	MA 51504	LSPQ
	MA 52535	LSPQ
	MA 52783	LSPQ
MSCNS (n = 17)	12228	ATCC
	14953	ATCC
	14990	ATCC
	15305	ATCC
	27836	ATCC
	27848	ATCC
	29070	ATCC
	29970	ATCC
	29974	ATCC
	35539	ATCC
	35552	ATCC
	35844	ATCC
	35982	ATCC
	43809	ATCC
	43867	ATCC
	43958	ATCC
	49168	ATCC

5

^a ATCC stands for "American Type Culture Collection".
LSPQ stands for "Laboratoire de Santé Publique du Québec".
CDC stands for "Center for Disease Control and Prevention".

Table 15. Clinical isolates used to test the sensitivity and/or specificity and/or ubiquity of the MRSA-specific PCR assays targeting MREJ sequences

Staphylococcal species	Number of strains	Source
MRSA (n = 177)	150	Canada
	10	China
	10	Denmark
	9	Argentina
	1	Egypt
	1	Sweden
	1	Poland
	3	Japan
	1	France
MSSA (n = 224)	208	Canada
	10	China
	4	Japan
	1	USA
	1	Argentina
MRCNS (n = 38)	32	Canada
	3	China
	1	France
	1	Argentina
	1	USA
MSCNS (n = 17)	14	UK
	3	Canada

Table 16. Analytical sensitivity of tests performed on a standard thermocycler using the set of primers targeting MREP types i, ii, iii, iv and v (SEQ ID NOs.: 64, 66, 67, 79 and 80) developed in the present invention for the detection and identification of MRSA

<i>Staphylococcus aureus</i> strain designation:		Detection limit (number of genome copies)
Original	CCRI ^a (MREP type)	
13370	CCRI-8894 (i)	10
ATCC 43300	CCRI-175 (ii)	5
9191	CCRI-2086 (ii)	10
35290	CCRI-1262 (iii)	5
352	CCRI-1266 (iii)	10
19121	CCRI-8895 (iv)	5
ATCC 33592	CCRI-178 (iv)	5
MA 50428	CCRI-1311 (v)	5
R991282	CCRI-2025 (v)	5

^a CCRI stands for "Collection of the Centre de Recherche en Infectiologie".

Table 17. Specificity and ubiquity tests performed on a standard thermocycler using the set of primers targeting MREP types i, ii, iii, iv and v (SEQ ID NO.: 64, 66, 67, 79 and 80) developed in the present invention for the detection and identification of MRSA

Strains	PCR results for SCCmec - <i>orfX</i> right extremity junction	
	Positive (%)	Negative (%)
MRSA - 35 strains ^a	27 (77.1)	8 (22.9)
MSSA - 44 strains	13 (29.5)	31 (70.5)
MRCNS - 9 strains*	0	9 (100)
MSCNS - 10 strains*	0	10 (100)

^a MRSA strains include the 20 strains listed in Table 3.

***Details regarding CNS strains:**

MRCNS : *S. caprae* (1)
S. cohnii cohnii (1)
S. epidermidis (1)
S. haemolyticus (2)
S. hominis (1)
S. sciuri (1)
S. simulans (1)
S. warneri (1)

MSCNS : *S. cohnii* (1)
S. epidermidis (1)
S. equorum (1)
S. haemolyticus (1)
S. lentus (1)
S. lugdunensis (1)
S. saccharolyticus (1)
S. saprophyticus (2)
S. xylosus (1)

Table 18. Analytical sensitivity of tests performed on the Smart
Cycler® thermocycler using the set of primers targeting
MREP types i, ii, iii, iv and v (SEQ ID NOs.: 64, 66,
67, 79 and 80) and molecular beacon probe (SEQ ID NO.:
84) developed in the present invention for the
detection and identification of MRSA

<i>Staphylococcus aureus</i> strain designation:		Detection limit (number of genome copies)
Original	CCRI ^a (MREP type)	
13370	CCRI-8894 (i)	2
ATCC 43300	CCRI-175 (ii)	2
9191	CCRI-2086 (ii)	10
35290	CCRI-1262 (iii)	2
352	CCRI-1266 (iii)	10
ATCC 33592	CCRI-178 (iv)	2
MA 51363	CCRI-1331 (iv)	5
19121	CCRI-8895 (iv)	10
Z109	CCRI-8903 (iv)	5
45302	CCRI-1263 (v)	10
MA 50428	CCRI-1311 (v)	5
MA 50609	CCRI-1312 (v)	5
MA 51651	CCRI-1325 (v)	10
39795-2	CCRI-1377 (v)	10
R991282	CCRI-2025 (v)	2

^a CCRI stands for "Collection of the Centre de Recherche en Infectiologie".

Table 19. Specificity and ubiquity tests performed on the Smart
Cycler[®] thermocycler using the set of primers targeting
MREP types i, ii, iii, iv and v (SEQ ID NO. : 64, 66,
67, 79 and 80) and molecular beacon probe (SEQ ID NO. :
84) developed in the present invention for the
detection of MRSA

Strains	PCR results for MREJ	
	Positive (%)	Negative (%)
MRSA - 29 strains ^a	21 (72.4)	8 (27.6)
MSSA - 35 strains	13 (37.1)	22 (62.9)
MRCNS - 14 strains	0	14 (100)
MSCNS - 10 strains	0	10 (100)

^a MRSA strains include the 20 strains listed in Table 3.

Details regarding CNS strains:

MRCNS : *S. epidermidis* (1)
S. haemolyticus (5)
S. simulans (5)
S. warneri (3)

MSCNS : *S. cohnii cohnii* (1)
S. epidermidis (1)
S. gallinarum (1)
S. haemolyticus (1)
S. lentus (1)
S. lugdunensis (1)
S. saccharolyticus (1)
S. saprophyticus (2)
S. xylosus (1)

Table 20. Analytical sensitivity of tests performed on the Smart Cyclor[®] thermocycler using the set of primers targeting MREP types i, ii, iii, iv, v and vii (SEQ ID NOs.: 64, 66, 67, 79 and 80) and molecular beacon probe (SEQ ID NO.: 84) developed in the present invention for the detection and identification of MRSA

<i>Staphylococcus aureus</i> strain designation:		Detection limit (number of genome copies)
Original	CCRI ^a (MREP type)	
13370	CCRI-8894 (i)	2
ATCC 43300	CCRI-175 (ii)	2
35290	CCRI-1262 (iii)	2
ATCC 33592	CCRI-178 (iv)	2
R991282	CCRI-2025 (v)	2
SE-41-1	CCRI-9771 (vii)	2

^a CCRI stands for "Collection of the Centre de Recherche en Infectiologie".

Table 21. Specificity and ubiquity tests performed on the Smart
Cycler[®] thermocycler using the set of primers targeting
MREP types i, ii, iii, iv, vi and vii (SEQ ID NOs.: 64,
66, 67, 79 and 80) and molecular beacon probe (SEQ ID
NO.: 84) developed in the present invention for the
detection and identification of MRSA

Strains	PCR results for MREJ	
	Positive (%)	Negative (%)
MRSA - 23 strains ^a	19 (82.6)	4 (17.4)
MSSA - 25 strains	13 (52)	12 (48)
MRCNS - 26 strains	0	26 (100)
MSCNS - 8 strains	0	8 (100)

^a MRSA strains include the 20 strains listed in Table 3.

Details regarding CNS strains:

MRCNS : *S. capitis* (2)
S. caprae (1)
S. cohnii (1)
S. epidermidis (9)
S. haemolyticus (5)
S. hominis (2)
S. saprophyticus (1)
S. sciuri (2)
S. simulans (1)
S. warneri (2)

MSCNS : *S. cohnii cohnii* (1)
S. epidermidis (1)
S. haemolyticus (1)
S. lugdunensis (1)
S. saccharolyticus (1)
S. saprophyticus (2)
S. xylosus (1)

Annex I: Strategy for the selection of specific amplification primers for types i and ii MREP

SEQ ID NO.:	Types i and ii MREP		orfx
	2324	2358	2583
2	TAT GTCAAAAATC ATGAACCTCA TTACTTATGA TA...CCT	TGTCAGGCC GTTTGATCCG CC	2607
1	TAT GTCAAAAATC ATGAACCTCA TTACTTATGA TA...CCT	TGTCAGGCC GTTTGATCCG CC	
17 ^a	TAT GTCAAAAATC ATGAACCTCA TTACTTATGA TA...CCT	TGTCAGGCC GTTTGATCCG CC	
18 ^a	TAT GTCAAAAATC ATGAACCTCA TTACTTATGA TA...CCT	TGTCAGGCC GTTTGATCCG CC	
19 ^a	TAT GTCAAAAATC ATGAACCTCA TTACTTATGA TA...CCT	TGTCAGGCC GTTTGATCCG CC	
20 ^a	TAT GTCAAAAATC ATGAACCTCA TTACTTATGA TA...CCT	TGTCAGGCC GTTTGATCCG CC	
21 ^a	TAT GTCAAAAATC ATGAACCTCA TTACTTATGA TA...CCT	TGTCAGGCC GTTTGATCCG CC	
22 ^a	TAT GTCAAAAATC ATGAACCTCA TTACTTATGA TA...CCT	TGTCAGGCC GTTTGATCCG CC	
23 ^a	TAT GTCAAAAATC ATGAACCTCA TTACTTATGA TA...CCT	TGTCAGGCC GTTTGATCCG CC	
24 ^a	TAT GTCAAAAATC ATGAACCTCA TTACTTATGA TA...CCT	TGTCAGGCC GTTTGATCCG CC	
25 ^a	TAT GTCAAAAATC ATGAACCTCA TTACTTATGA TA...CCT	TGTCAGGCC GTTTGATCCG CC	
26	TAT GTCAAAAATC ATGAACCTCA TTACTTATGA TA...CCT	TGTCAGGCC GTTTGATCCG CC	
33 ^c		CtT gGTGtAaaCC aTTgAgCCa CC	
34 ^c		CCT caTGAaAtCC aTTGATC	

Selected sequence
for type i MREP
and ii primer
(SEQ ID No.: 66)

GTCAAAAATC ATGAACCTCA TTACTTATG

Selected sequence
for orfx primer^b
(SEQ ID NO.: 64)

TGTCAGGCC GTTTGATCC

The sequence positions refer to SEQ ID NO.: 2.

Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the displayed sequences.

^a These sequences are the reverse-complements of SEQ ID NOs.: 17-25.

^b This sequence is the reverse-complement of the selected primer.

^c SEQ ID NOs.: 33 and 34 were obtained from CNS species.

Annex II: Strategy for the selection of a specific molecular beacon probe for the real-time detection of MREJ

SEQ ID NO. :	327	<u>orfX</u>	371
165	ACAAG GACGT	CTTACAACGC AGTAAC	TATG CACTA
180	ACAAG GACGT	CTTACAACGC AGTAAC	TATG CACTA
181	ACAAG GACGT	CTTACAACGC AGTAAC	TATG CACTA
182	ACAAG GACGT	CTTACAACGC AGTAAC	TATG CACTA
183	ACAAG GACGT	CTTACAACGC AGTAAC	TATG CACTA
184	ACAAG GACGT	CTTACAACGC AGTAAC	TATG CACTA
186	ACAAG GACGT	CTTACAACGC AGTAAC	TATG CACTA
174	ACAAG GACGT	CTTACAACGC AGTAAC	TATG CACTA
175	ACAAG GACGT	CTTACAACGC AGTAAC	TATG CACTA
178	ACAAG GACGT	CTTACAACGC AGTAAC	TATG CACTA
176	ACAAG GACGT	CTTACAACGC AGTAAC	TATG CACTA
173	ACAAG GACGT	CTTACAACGC AGTAAC	TATG CACTA
177	ACAAG GACGT	CTTACAACGC AGTAAC	TATG CACTA
169	ACAAG GACGT	CTTACAACGC AGTAAC	TATG CACTA
199	ACAAG GACGT	CTTACAACGC AGTAAC	TATG CACTA
33 ^{a,b}	ACcAa GACGT	CTTACAACGC AGcAAC	TATG CttTA
34 ^{a,b}	AtgAG GACGT	CTTACAACGC AGcAAC	TATG CACTt

Selected sequence
for orfX molecular
beacon probes
(SEQ ID NO.:163)^c
(SEQ ID NO.:164)^c
(SEQ ID NO.: 84)^c

GACGT CTTACAACGC AGTAAC

TATG

GACGT CTTACAACGC AGTAAC

TATG

GACGT CTTACAACGC AGTAAC

TATG

Nucleotide discrepancies between the orfX sequences and SEQ ID NO.: 84 are shown in lower-case. Other entries in the sequence listing also present similar variations. The stem of the molecular beacon probes are not shown for sake of clarity. The sequence positions refer to SEQ ID NO.:165.

^a These sequences are the reverse-complements of SEQ ID NOs.: 33 and 34.

^b SEQ ID NOs.: 33 and 34 were obtained from CNS species.

^c The sequences presented are the reverse-complement of the selected molecular beacon probes.

CLAIMS

What is claimed is :

- 5 1. A method to detect the presence of a methicillin-resistant *Staphylococcus aureus* (MRSA) strain in a sample, said MRSA strain being resistant because of the presence of an SCCmec insert containing a *mecA* gene, said SCCmec being inserted in bacterial nucleic acids thereby generating a polymorphic right extremity junction (MREJ), said method comprising the step of annealing the nucleic acids of the sample with a plurality of probes
10 and/or primers, characterized by:
- (i) said primers and/or probes are specific for MRSA strains and capable of annealing with polymorphic MREJ nucleic acids, said polymorphic MREJ comprising MREJ types i to x; and
15 (ii) said primers and/or probes altogether can anneal with at least four MREJ types selected from MREJ types i to x.
2. The method of claim 1, wherein the primers and/or probes are all chosen to anneal under common annealing conditions.
20
3. The method of claim 2, wherein the primer and/or probes are placed altogether in the same physical enclosure.
4. The method of any one of claims 1 to 3, wherein the primers and/or probes have at
25 least 10 nucleotides in length and are capable of annealing with MREJ types i to iii, defined in any one of SEQ ID NOs: 1, 20, 21, 22, 23, 24, 25, 41, 199 ; 2, 17, 18, 19, 26, 40, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 185, 186, 197 ; 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 104, 184, 198 ;
and with one or more of MREJ types iv to ix, having SEQ ID NOs: 42, 43, 44, 45, 46, 51 ;
30 47, 48, 49, 50 ; 171 ; 165, 166 ; 167 ; 168.
5. The method of any one of claims 1 to 4, wherein the primers and/or probes altogether can anneal with said SEQ ID NOs of MREJ types i to ix.

6. The method of any one of claims 1 to 5, wherein said primers and/or probes have the following sequences SEQ ID NOs:

5 66, 100, 101, 105, 52, 53, 54, 55, for the detection of MREJ type i
 56, 57, 64, 71, 72, 73, 74, 75, 76,
 70, 103, 130, 132, 158, 159, 59,
 62, 126, 127, 128, 129, 131, 200,
 201, 60, 61, 63
 10 32, 83, 84, 160, 161, 162, 163, 164
 85, 86, 87, 88, 89

66, 97, 99, 100, 101, 106, 117, for the detection of MREJ type ii
 118, 124, 125, 52, 53, 54, 55, 56, 57
 15 64, 71, 72, 73, 74, 75, 76, 70,
 103, 130, 132, 158, 159
 59, 62
 126, 127
 128, 129, 131, 200, 201
 20 60, 61, 63
 32, 83, 84, 160, 161, 162, 163, 164
 85, 86, 87, 88, 89

67, 98, 102, 107, 108 for the detection of MREJ type iii
 25 64, 71, 72, 73, 74, 75, 76, 70,
 103, 130, 132, 158, 159
 58,
 59, 62
 126, 127
 30 128, 129, 131, 200, 201
 60, 61, 63
 32, 83, 84, 160, 161, 162, 163, 164
 85, 86, 87, 88, 89

35 79, 77, 145, 147 for the detection of MREJ type iv
 64, 71, 72, 73, 74, 75, 76, 70,
 103, 130, 132, 158, 159
 59, 62
 126, 127
 40 128, 129, 131, 200, 201
 60, 61, 63
 68
 32, 83, 84, 160, 161, 162, 163, 164
 85, 86, 87, 88, 89

45 65, 80, 146, 154, 155 for the detection of MREJ type v
 64, 71, 72, 73, 74, 75, 76,
 70, 103, 130, 132, 158, 159
 59, 62
 50 126, 127

128, 129, 131, 200, 201
 60, 61, 63
 32, 83, 84, 160, 161, 162, 163, 164
 85, 86, 87, 88, 89

5

202, 203, 204 for the detection of MREJ type vi
 64, 71, 72, 73, 74, 75, 76, 70,
 103, 130, 132, 158, 159
 59, 62

10

126, 127
 128, 129, 131, 200, 201
 60, 61, 63
 32, 83, 84, 160, 161, 162, 163, 164
 85, 86, 87, 88, 89

15

112, 113, 114, 119, 120, 121, 122 for the detection of MREJ type vii
 , 123, 150, 151, 153
 64, 71, 72, 73, 74, 75, 76, 70, 103,
 130, 132, 158, 159

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59, 62
 126, 127
 128, 129, 131, 200, 201
 60, 61, 63
 32, 83, 84, 160, 161, 162, 163, 164

25

85, 86, 87, 88, 89

115, 116, 187, 188, 207, 208 for the detection of MREJ type viii
 64, 71, 72, 73, 74, 75, 76, 70,
 103, 130, 132, 158, 159

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59, 62
 126, 127
 128, 129, 131, 200, 201
 60, 61, 63
 32, 83, 84, 160, 161, 162, 163, 164

35

85, 86, 87, 88, 89

109, 148, 149, 205, 206 for the detection of MREJ type ix.
 64, 71, 72, 73, 74, 75, 76
 70, 103, 130, 132, 158, 159

40

59, 62
 126, 127
 128, 129, 131, 200, 201
 60, 61, 63
 32, 83, 84, 160, 161, 162, 163, 164

45

85, 86, 87, 88, 89

7. The method of claim 6, wherein primer pairs have the nucleotide sequence which are defined in SEQ ID NOs :

50

- 64/66, 64/100, 64/101; 59/52, 59/53, 59/54, 59/55, 59/56, 59/57, 60/52, 60/53, 60/54, 60/55, 60/56 5 60/57, 61/52, 61/53, 61/54, 61/55 61/56, 61/57, 62/52, 62/53, 62/54 62/55, 62/56, 62/57, 63/52, 63/53 63/54, 63/55, 63/56, 63/57
- 64/66, 64/97, 64/99, 64/100, 64/101 10 59/52, 59/53, 59/54, 59/55, 59/56, 59/57, 60/52, 60/53, 60/54, 60/55, 60/56, 60/57, 61/52, 61/53, 61/54, 61/55, 61/56, 61/57, 62/52, 62/53, 62/54, 62/55, 62/56, 62/57, 63/52 15 63/53, 63/54, 63/55, 63/56, 63/57
- 64/67, 64/98, 64/102 ; 59/58, 60/58, 61/58, 62/58, 63/58 for the detection of type iii MREJ
- 20 64/79 for the detection of type iv MREJ 64/80 for the detection of type v MREJ 64/204 for the detection of type vi MREJ 64/112, 64/113 for the detection of type vii MREJ 64/115, 64/116 for the detection of type viii MREJ 25 64/109 for the detection of type ix MREJ
8. The method of claim 7, further comprising probes having the following sequences:
30 SEQ ID NOs: 32, 83, 84, 160, 161, 162, 163, 164 for the detection of MREJ types i to ix.
9. The method of any one of claims 6 to 8, wherein said primers and probes have the following nucleotide sequences:
- 35 vii) SEQ ID NOs: 64, 66, 84, 163, 164 for the detection of MREJ type i viii) SEQ ID NOs: 64, 66, 84, 163, 164 for the detection of MREJ type ii ix) SEQ ID NOs: 64, 67, 84, 163, 164 for the detection of MREJ type iii x) SEQ ID NOs: 64, 79, 84, 163, 164 for the detection of MREJ type iv xi) SEQ ID NOs: 64, 80, 84, 163, 164 for the detection of MREJ type v xii) SEQ ID NOs: 64, 112, 84, 163, 164 for the detection of MREJ type vii.
- 40 10. The method of any one of claims 1 to 8, wherein said probes and primers are used together.

11. The method of claim 9 or 10, wherein said probes and/or primers are used together in the same physical enclosure.

12. A method for typing a MREJ of a MRSA strain, which comprises the steps of:

5 reproducing the method of any one of claims 1 to 11 with primers and/or probes specific for a determined MREJ type, and detecting an annealed probe and/or primer as an indication of the presence of a determined MREJ type.

10 13. A nucleic acid selected from:

vii) SEQ ID NOs: 42, 43, 44, 45, 46, 51 for sequence of MREJ type iv ;

viii) SEQ ID NOs: 47, 48, 49, 50 for sequence of MREJ type v ;

ix) SEQ ID NOs: 171 for sequence of MREJ type vi ;

x) SEQ ID NOs: 165, 166 for sequence of MREJ type vii ;

15 xi) SEQ ID NOs: 167 for sequence of MREJ type viii ;

xii) SEQ ID NOs: 168 for sequence of MREJ type ix.

14. An oligonucleotide of at least 10 nucleotides in length which hybridizes with the nucleic acid of claim 13 and which hybridizes with one or more MREJ of types selected
20 from iv to ix.

15. An oligonucleotide pair which has the nucleotide sequences defined in any one of SEQ ID NOs:

25 64/66, 64/100, 64/101; 59/52, for the detection of type i MREJ
59/53, 59/54, 59/55, 59/56, 59/57,
60/52, 60/53, 60/54, 60/55, 60/56
60/57, 61/52, 61/53, 61/54, 61/55
61/56, 61/57, 62/52, 62/53, 62/54
30 62/55, 62/56, 62/57, 63/52, 63/53
63/54, 63/55, 63/56, 63/57

64/66, 64/97, 64/99, 64/100, 64/101 for the detection of type ii MREJ
59/52, 59/53, 59/54, 59/55, 59/56,
35 59/57, 60/52, 60/53, 60/54, 60/55,
60/56, 60/57, 61/52, 61/53, 61/54,
61/55, 61/56, 61/57, 62/52, 62/53,
62/54, 62/55, 62/56, 62/57, 63/52
63/53, 63/54, 63/55, 63/56, 63/57
40

64/67, 64/98, 64/102 ; 59/58,
60/58, 61/58, 62/58, 63/58

for the detection of type iii MREJ

64/79

for the detection of type iv MREJ

5 64/80

for the detection of type v MREJ

64/204

for the detection of type vi MREJ

64/112, 64/113

for the detection of type vii MREJ

64/115, 64/116

for the detection of type viii MREJ

64/109

for the detection of type ix MREJ

10

16. An oligonucleotide which has the nucleotide sequence defined in any one of SEQ ID
15 NOs: 32, 83, 84, 160, 161, 162, 163, 164.

17. A composition of matter comprising primers and/or probes, the nucleotide sequences
of which have at least 10 nucleotides in length which hybridize with any nucleic acid defined
in claim 13, and which hybridize with one or more MREJ of types selected from iv to ix.

20

18. The composition of claim 17, which further comprises primers and/or probes, which
hybridize with one or more MREJ of types selected from i to iii.

19. The composition of claim 18 or 19, wherein the primers pairs have the nucleotide
25 sequences defined in SEQ ID NOs:

64/66, 64/100, 64/101; 59/52,
59/53, 59/54, 59/55, 59/56, 59/57,
60/52, 60/53, 60/54, 60/55, 60/56
30 60/57, 61/52, 61/53, 61/54, 61/55
61/56, 61/57, 62/52, 62/53, 62/54
62/55, 62/56, 62/57, 63/52, 63/53
63/54, 63/55, 63/56, 63/57

for the detection of type i MREJ

64/66, 64/97, 64/99, 64/100, 64/101
59/52, 59/53, 59/54, 59/55, 59/56,
59/57, 60/52, 60/53, 60/54, 60/55,
60/56, 60/57, 61/52, 61/53, 61/54,
61/55, 61/56, 61/57, 62/52, 62/53,
40 62/54, 62/55, 62/56, 62/57, 63/52
63/53, 63/54, 63/55, 63/56, 63/57

for the detection of type ii MREJ

64/67, 64/98, 64/102 ; 59/58,
60/58, 61/58, 62/58, 63/58

for the detection of type iii MREJ

64/79

for the detection of type iv MREJ

5 64/80

for the detection of type v MREJ

64/204

for the detection of type vi MREJ

64/112, 64/113

for the detection of type vii MREJ

64/115, 64/116

for the detection of type viii MREJ

64/109

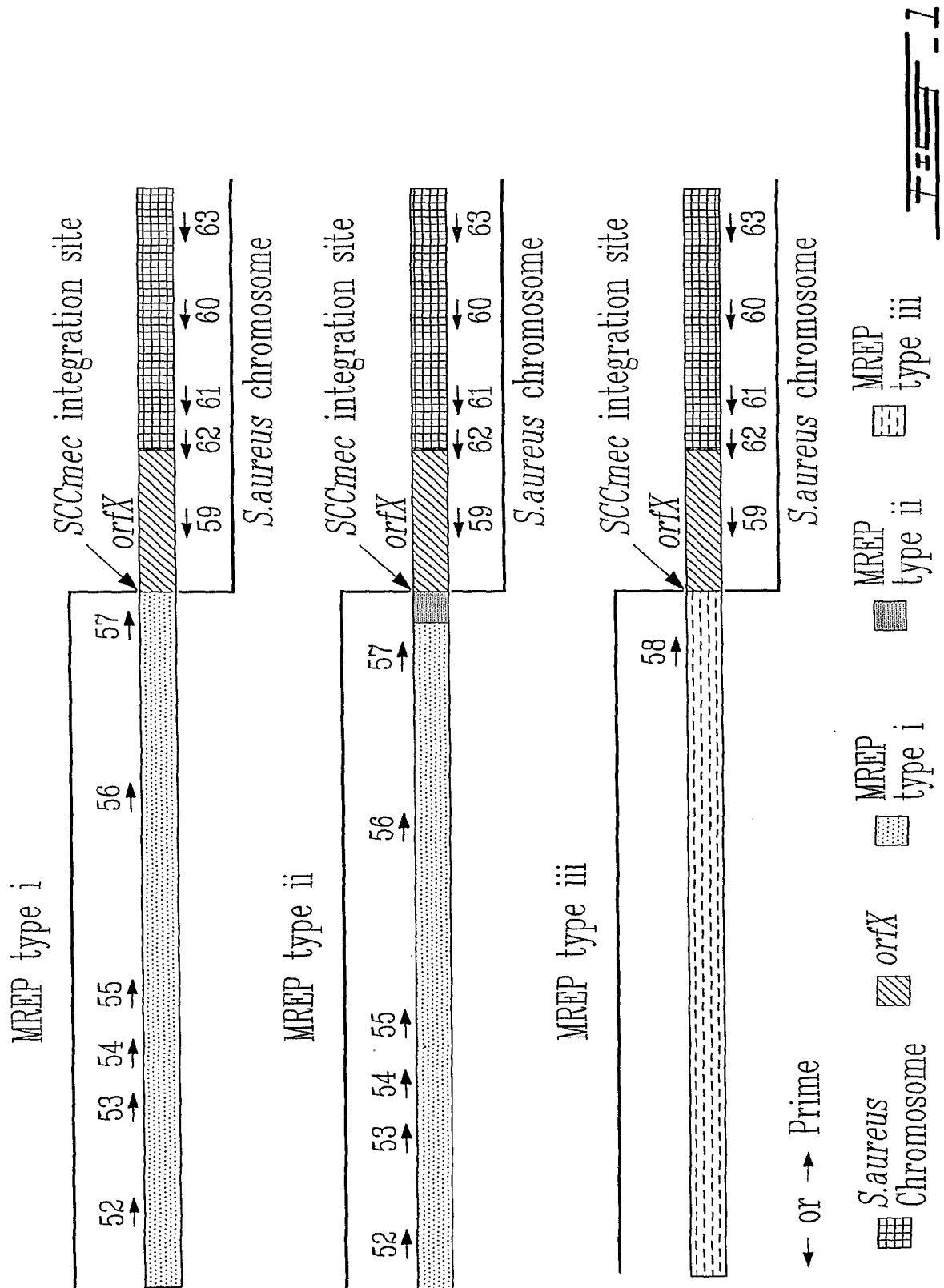
for the detection of type ix MREJ

10

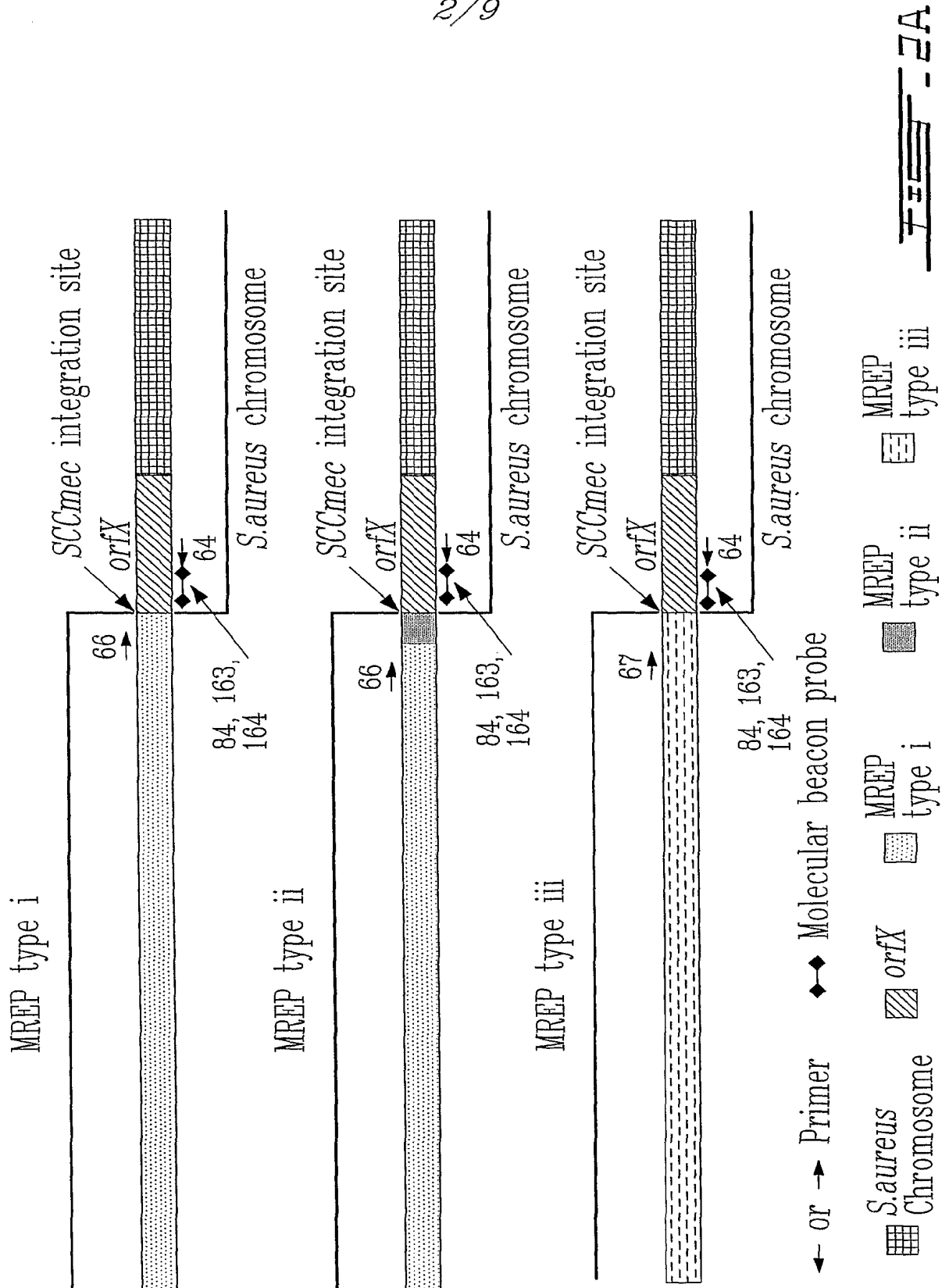
20. The composition of claim 18, which further comprises probes, which SEQ ID NOs are: 32, 83, 84, 160, 161, 162, 163, 164.

15

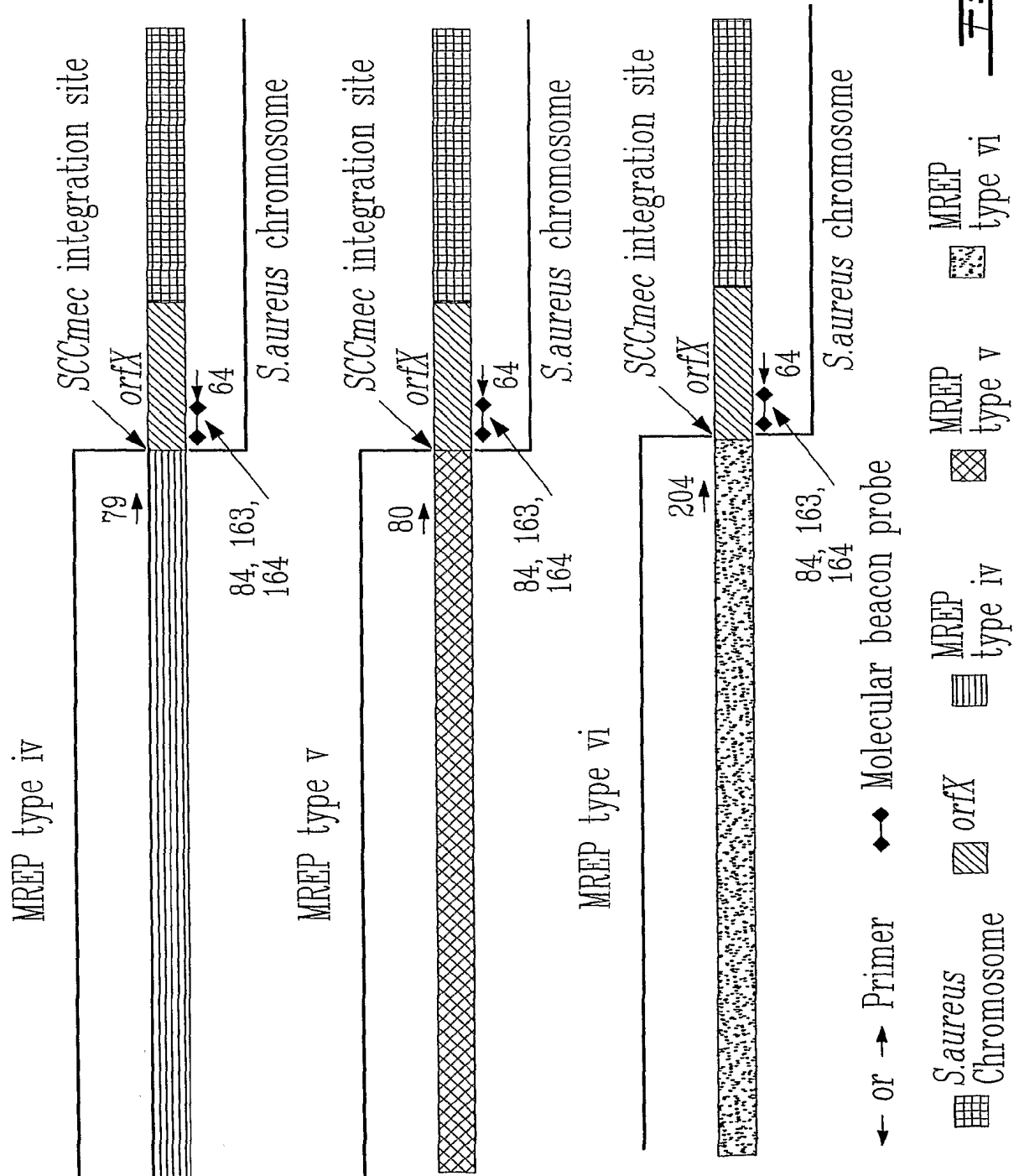
1/9



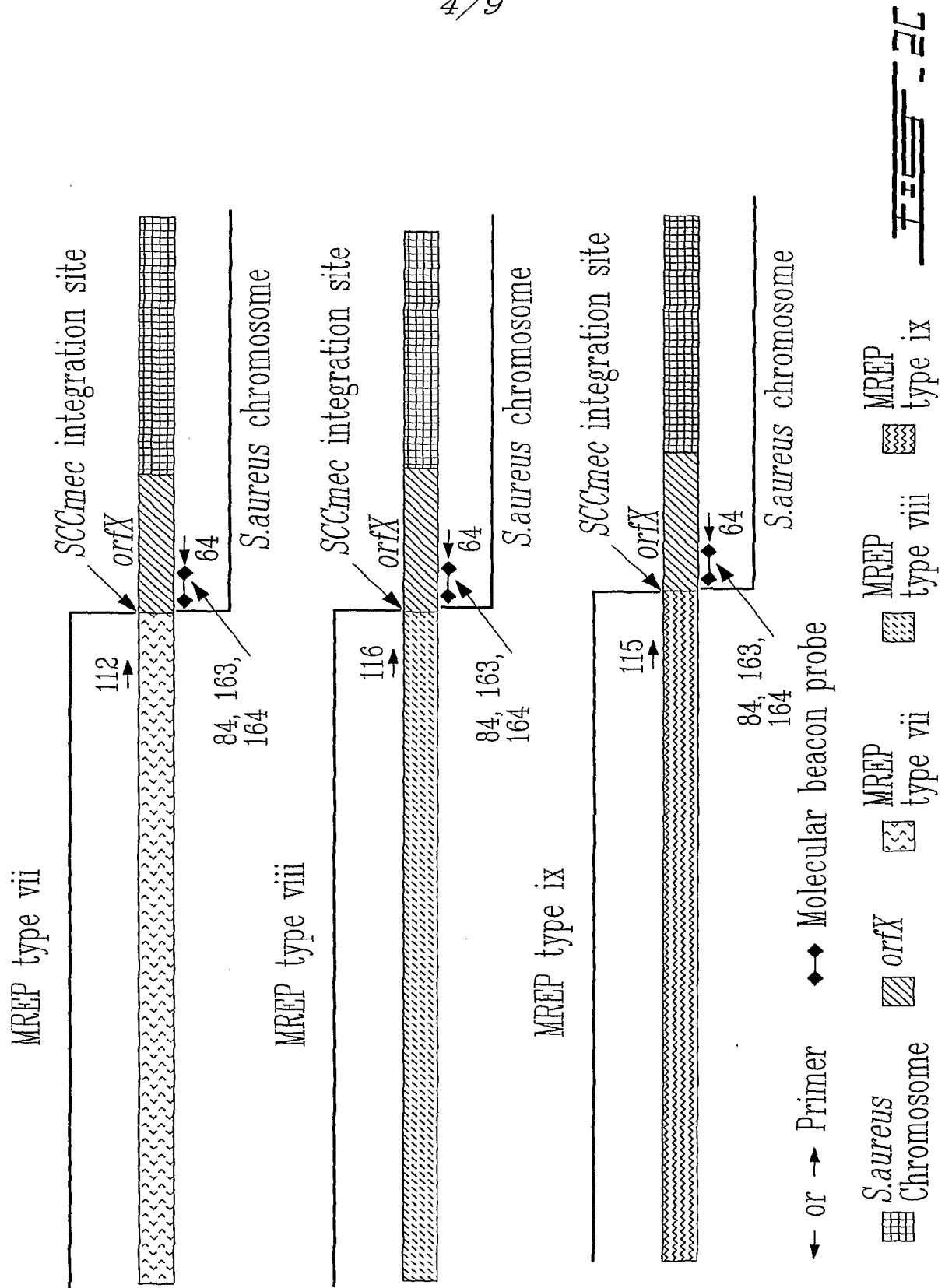
2/9



3/9



4/9



5/9

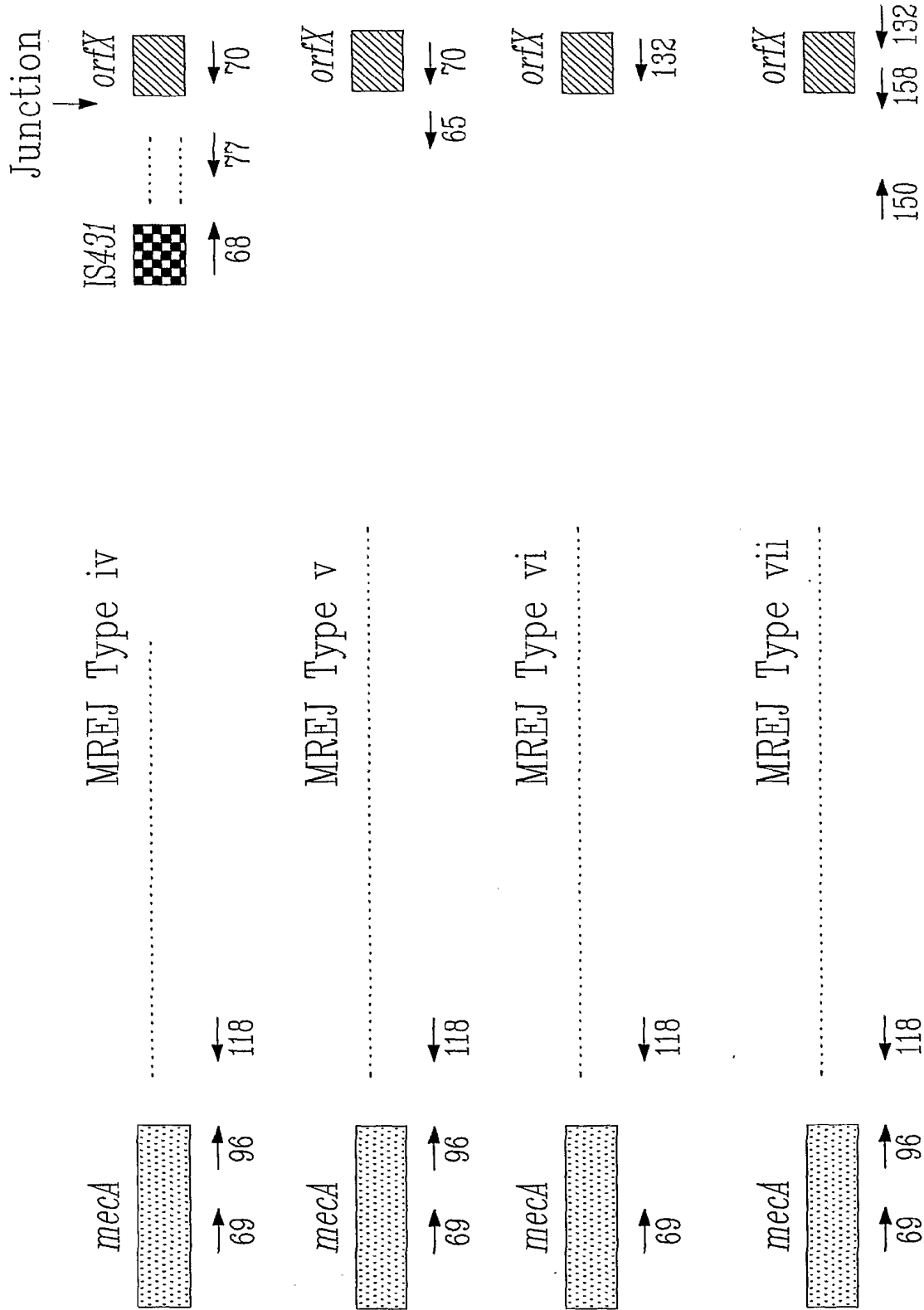
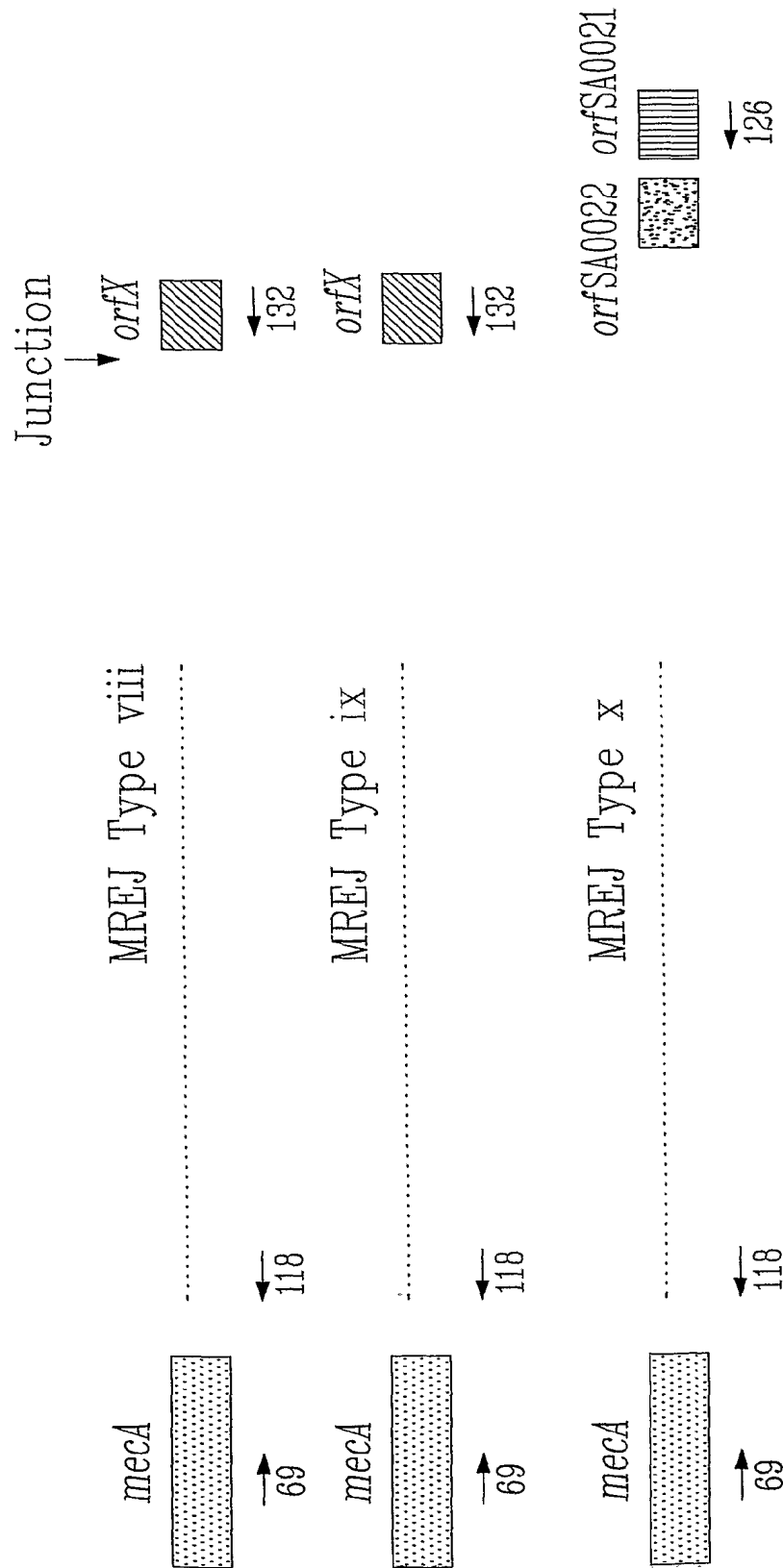


FIG. 3A



Primer \rightarrow or \leftarrow

五、五

8/9

201

Type iii
Type vii
Type vi
Type i
Type ii
Type ix
Type viii
Type v
Type iv

300

301
 Type iii ATAAAGCA GTTATTACG
 Type vii TGAATTCC TCGCTACG
 Type vi GGTATCATA TCGCTCAGCA
 Type i AGAAGATCG ACAATGATTA
 Type ii AGAAGATCG ACAATGATTA
 Type ix TAAATACACA TAAATACACA
 Type viii TTTACAAAG CACTATACAC
 Type v TTAAAGATAT CATTAATTT
 Type iv ATATTACAT TATTAGAGCT

Feb. 4th

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS:

HULETSKY, Ann ¹, 1231 Av des Pins, Sillery, Quebec,
Canada, G1S 4J3

ROSSBACH, Valery ¹, 55 Rue du Sauternes, Aylmer,
Quebec, Canada, J9H 3W7

¹:Canadian citizenship

(ii) TITLE OF THE INVENTION: SEQUENCES FOR DETECTION AND
IDENTIFICATION OF METHICILLIN-RESISTANT STAPHYLOCOCCUS
AUREUS

(iii) NUMBER OF SEQUENCES: 233

(iv) CORRESPONDENCE ADDRESS:

(A)	ADDRESSEE:
(B)	STREET:
(C)	CITY:
(D)	STATE:
(E)	COUNTRY:
(F)	ZIP:

(v) COMPUTER READABLE:

(A)	MEDIUM TYPE:
(B)	COMPUTER:
(C)	OPERATING:
(D)	SOFTWARE:

(vi) CURRENT APPLICATION DATA:

(A)	APPLICATION:
(B)	FILING DATE:
(C)	CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A)	APPLICATION:
(B)	FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A)

NAME:

(B)

REGISTRATION NUMBER:

(ix) TELECOMMUNICATION INFORMATION:

(A)

TELEPHONE:

(B)

TELEFAX:

2) INFORMATION FOR SEQ ID NO: 1

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3050 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: NCTC 10442
- (C) ACCESSION NUMBER: Extracted from AB033763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1

TCGTGCCATT	GATGCAGAGG	GACATACATT	AGATATTTGG	TTGCGTAAGC	50
AACGAGATAA	TCATTCAGCA	TATGCGTTTA	TCAAACGTCT	CATTAAACAA	100
TTTGGTAAAC	CTCAAAGGT	AATTACAGAT	CAGGCACCTT	CAACGAAGGT	150
AGCAATGGCT	AAAGTAATTA	AAGCTTTTAA	ACTTAAACCT	GACTGTCATT	200
GTACATCGAA	ATATCTGAAT	AACCTCATTG	AGCAAGATCA	CCGTCATATT	250
AAAGTAAGAA	AGACAAGGTA	TCAAAGTATC	AATACAGCAA	AGAATACTTT	300
AAAAGGTATT	GAATGTATTT	ACGCTCTATA	TAAAAAGAAC	CGCAGGTCTC	350
TTCAGATCTA	CGGATTTTCG	CCATGCCACG	AAATTAGCAT	CATGCTAGCA	400
AGTTAAGCGA	ACACTGACAT	GATAAATTAG	TGGTTAGCTA	TATTTTTTTA	450
CTTTGCAACA	GAACCGAAAA	TAATCTCTTC	AATTTATTTT	TATATGAATC	500
CTGTGACTCA	ATGATTGTAA	TATCTAAAGA	TTTCAGTTCA	TCATAGACAA	550
TGTTCTTTTC	AACATTTTTT	ATAGCAAATT	GATTAAATAA	ATTCTCTAAT	600
TTCTCCCGTT	TGATTTCACT	ACCATAGATT	ATATTATCAT	TGATATAGTC	650
AATGAATAAT	GACAAATTAT	CACTCATAAC	AGTCCCAACC	CCTTTATTTT	700
GATAGACTAA	TTATCTTCAT	CATTGTAAAA	CAAATTACAC	CCTTTAAATT	750
TAACTCAACT	TAAATATCGA	CAAATTAATA	AACAATAAAA	TTACTTGAAT	800
ATTATTCATA	ATATATTAAC	AACTTTATTA	TACTGCTCTT	TATATATAAA	850
ATCATTAATA	ATTAAACAAG	CCTTAAATAA	TTTAACTTTT	TTGTGATTAT	900
TACACATTAT	CTTATCTGCT	CTTTATCACC	ATAAAAATAG	AAAAACAAG	950
ATTCCTAAAG	AATATAGGAA	TCTTGTTTCA	GACTGTGGAC	AAACTGATTT	1000
TTTATCAGTT	AGCTTATTTA	GAAAGTTTTA	TTTAAATTAC	AGTTTCTATT	1050
TTTATTAGAT	CACAATTTTA	TTTTAGCTCT	TGTTCAAGTA	ATCATTTTTTC	1100
GCCAAAAACT	TTATACTGAA	TAGCTTCTAC	ATTAAATACT	TTGTCAATGA	1150
GATCATCTAC	ATCTTTAAAT	TCAGAATAAT	TTGCATATGG	ATCTATAAAA	1200
TAAAATTGTG	GTTCTTTACC	GGAAACATTA	AATATTCTTA	ATATTAAATA	1250
TTTCTGCTTA	TATTCTTTCA	TAGCAAACAT	TTCATTTAGC	GACATAAAAA	1300
ATGGTTCCTC	AATACTAGAA	GATGTAGATG	TTTTAATTTT	AATAAATTTT	1350
TCTACAGCTT	TATCTGTATT	TGTTGGATCA	AAAGCTACTA	AATCATAGCC	1400
ATGACCGTGT	TGAGAGCCTG	GATTATCATT	TAAAATATTC	CTAAACTGTT	1450
CTTCTTATC	TTCGTCTATT	TTATTATCAA	TTAGCTCATT	AAAGTAATTT	1500
AGCGCTAATT	TTTCTCCAAC	TTTACCGGTT	AATTTATTCT	CTTTATTTGA	1550
TTTTTCAATT	TCTGAATCAT	TTTTAGTAGT	CTTTGATACA	CCTTTTTTTAT	1600
ATTTTGGAAT	TATTCCTTTA	GGTGCTTCCA	CTTCCTTGAG	TGTCTTATCT	1650
TTTTGTGCTG	TTCTAATTTT	TTCAATTTTC	CTGTCTTCCT	GTATTTTCGTC	1700
TATGCTATTG	ACCAAGCTAT	CATAGGATGT	TTTTGTAACT	TTTGAAGCTA	1750

ATTCATTAAA	TAGTTCTAAA	AATTTCTTTA	AATCCTCTAG	CATATCTTCT	1800
TCTGTGAATC	CTTCATTCAA	ATCATAATAT	TTGAATCTTA	TTGATCCATG	1850
AGAATATCCT	GATGGATAAT	CATTTTTTTAA	ATCATAAGAT	GAATCTTTAT	1900
TTTCTGCGTA	ATAAAATCTT	CCAGTATTAA	ATTCATTTGA	TGTAATATAT	1950
TTATTGAGTT	CGGAAGATAA	AGTTAATGCT	CTTTGTTTTG	CAGCATTTTT	2000
ATCCCGCGGA	AACATATCAC	TTATCTTTGA	CCATCCTTGA	TTCAAAGATA	2050
AGTATATGCC	TTCTCCTTCC	GGATGAAAAA	GATATACCAA	ATAATATCCA	2100
TCCTTTGTTT	CTTTTGTTAT	ATTCTCATCA	TATATTGAAA	TCCAAGGAAC	2150
TTTACTATAG	TTCCCAGTAG	CAACCTTCCC	TACAAC TGAA	TATTTATCTT	2200
CTTTTATATG	CACTTTTAAAC	TGCTTG GGTG	ACTTATCATG	GACTAAAGTT	2250
TTATATAGAT	CACCTTTATC	CCAATCAGAT	TTTTTAACTA	CATTATTGGT	2300
ACGTTTCTCT	TTAATTAATT	TAAGGACCTG	CATAAAGTTG	TCTATCATTT	2350
GAAATTCCCT	CCTATTATAA	AATATATTAT	GTCTCATTTT	CTTCAATATG	2400
TACTTATTTA	TATTTTACCG	TAATTTACTA	TATTTAGTTG	CAGAAAGAAT	2450
TTTCTCAAAG	CTAGAACTTT	GCTTCACTAT	AAGTATTCAG	TATAAAGAAT	2500
ATTTGCTAT	TATTTACTTG	AAATGAAAGA	CTGCGGAGGC	TAACATATGTC	2550
AAAAATCATG	AACCTCATTA	CTTATGATAA	GCTTCTCCTC	GCATAATCTT	2600
AAATGCTCTG	TACACTTGTT	CAATTAACAC	AACCCGCATC	ATTTGATGTG	2650
GGAATGTCAT	TTTGCTGAAT	GATAGTGCGT	AGTTACTGCG	TTGTAAGACG	2700
TCCTTG TGCA	GGCCGTTTGA	TCCGCCAATG	ACGAAAACAA	AGTCGCTTTG	2750
CCCTTG GGTG	ATGCGTTGGT	TCAATTCTTG	GGCCAATCCT	TCGGAAGATA	2800
GCATCTTTCC	TTGTATTTCT	AATGTAATGA	CTGTGGATTG	TGGTTTGATT	2850
TTGGCTAGTA	TTCGTTGGCC	TTCTTTTTTCT	TTTACTTGCT	CAATTTCTTT	2900
GTCACTCATA	TTTTCTGGTG	CTTTTTCGTC	TGGAAC TTCT	ATGATGTCTA	2950
TCTTGGTGTA	TGGGCCTAAA	CGTTTTTTCAT	ATTCTGCTAT	GGCTTGCTTC	3000
CAATATTTCT	CTTTTAGTTT	CCCTACAGCT	AAAATGGTGA	TTTTTCATGTC	3050

2) INFORMATION FOR SEQ ID NO: 2

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3050 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: N315
- (C) ACCESSION NUMBER: Extracted from D86934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2

ACCTCATTTGA	GCAAGATCAC	CGTCATATTA	AAGTAAGAAA	GACAAGGTAT	50
CAAAGTATCA	ATACAGCAAA	GAATACTTTA	AAAGGTATTG	AATGTATTTA	100
CGCTCTATAT	AAAAAGAACC	GCAGGTCTCT	TCAGATCTAC	GGATTTTCGC	150
CATGCCACGA	AATTAGCATC	ATGCTAGCAA	GTTAAGCGAA	CACTGACATG	200
ATAAATTAGT	GGTTAGCTAT	ATTTTTTTTAC	TTTGCAACAG	AACCGAAAAT	250
AATCTCTTCA	ATTTATTTTT	ATATGAATCC	TGTGACTCAA	TGATTGTAAT	300

ATCTAAAGAT	TTCAGTTCAT	CATAGACAAT	GTTCTTTTCA	ACATTTTTTTA	350
TAGCAAATTG	ATTAAATAAA	TTCTCTAATT	TCTCCCGTTT	GATTTCACTA	400
CCATAGATTA	TATTATCATT	GATATAGTCA	ATGAATAATG	ACAAATTATC	450
ACTCATAACA	GTCCCAACCC	CTTTCTTTTG	ATAGACTAAT	TATCTTCATC	500
ATTGTAAAC	AAATTACACC	CTTTAAATTT	AACTCAACTT	AAATATCGAC	550
AAATTAAAAA	ACAATAAAAT	TACTTGAATA	TTATTCATAA	TATATTAACA	600
ACTTTATTAT	ACTGCTCTTT	ATATATAAAA	TCATTAATAA	TTAAACAAGC	650
CTTAAAATAT	TTAACTTTTT	TGTGATTATT	ACACATTATC	TTATCTGCTC	700
TTTATCACCA	TAAAAATAGA	AAAAACAAGA	TTCTTAAAGA	ATATAGGAAT	750
CTTGTTTCAG	ACTGTGGACA	AACTGATTTT	TTATCAGTTA	GCTTATTTAG	800
AAAGTTTTAT	TTAAATTACA	GTTTCTATTT	TTATTAGATC	ACAATTTTAT	850
TTTAGCTCTT	GTTCAAGTAA	TCATTTTTCG	CCAAAAACTT	TATACTGAAT	900
AGCTTCTACA	TTAAATACTT	TGTCAATGAG	ATCATCTACA	TCTTTAAATT	950
CAGAATAATT	TGCATATGGA	TCTATAAAAT	AAAATTGTGG	TTCTTTACCG	1000
GAAACATTAA	ATATTCTTAA	TATTAAATAT	TTCTGCTTAT	ATTCTTTCAT	1050
AGCAAACATT	TCATTTAGCG	ACATAAAAAA	TGGTTCCTCA	ATACTAGAAG	1100
ATGTAGATGT	TTTAATTTCA	ATAAATTTTT	CTACAGCTTT	ATCTGTATTT	1150
GTTGGATCAA	AAGCTACTAA	ATCATAGCCA	TGACCGTGTT	GAGAGCCTGG	1200
ATTATCATTT	AAAATATTCC	TAAACTGTTC	TTTCTTATCT	TCGTCTATTT	1250
TATTATCAAT	TAGCTCATTA	AAGTAATTTA	GCGCTAATTT	TTCTCCAAC	1300
TTACCGGTTA	ATTTATTCTC	TTTATTTGAT	TTTTCAATTT	CTGAATCATT	1350
TTTAGTAGTC	TTTGATACAC	CTTTTTTATA	TTTTGGAATT	ATTCCTTTAG	1400
GTGCTTCCAC	TTCTTGAGT	GTCTTATCTT	TTTGTGCTGT	TCTAATTTCT	1450
TCAATTTTCGC	TGTCTTCCTG	TATTTTCGTCT	ATGCTATTGA	CCAAGCTATC	1500
ATAGGATGTT	TTTGTAAGT	TTGAAGCTAA	TTCAATTAAAT	AGTTCTAAAA	1550
ATTTCTTTAA	ATCCTCTAGC	ATATCTTCTT	CTGTGAATCC	TTCATTCAAA	1600
TCATAATATT	TGAATCTTAT	TGATCCATGA	GAATATCCTG	ATGGATAATC	1650
ATTTTTTTAA	TCATAAGATG	AATCTTTATT	TTCTGCGTAA	TAAAATCTTC	1700
CAGTATTAAA	TTCAATTTGAT	GTAATATATT	TATTGAGTTC	GGAAGATAAA	1750
GTTAATGCTC	TTTGTTTTGC	AGCATTTTTTA	TCCCGCGGAA	ACATATCACT	1800
TATCTTTGAC	CATCCTTGAT	TCAAAGATAA	GTATATGCCT	TCTCCTTCCG	1850
GATGAAAAAG	ATATACCAAA	TAATATCCAT	CCTTTGT TTC	TTTTGTTATA	1900
TTCTCATCAT	ATATTGAAAT	CCAAGGAAC	TTACTATAGT	TCCCAGTAGC	1950
AACCTTCCCT	ACAACCTGAAT	ATTTATCTTC	TTTTATATGC	ACTTTTAACT	2000
GCTTGGGTAA	CTTATCATGG	ACTAAAGTTT	TATATAGATC	ACCTTTATCC	2050
CAATCAGATT	TTTTAACTAC	ATTATTGGTA	CGTTTCTCTT	TAATTAATTT	2100
AAGGACCTGC	ATAAAGTTGT	CTATCATTTG	AAATTCCCTC	CTATTATAAA	2150
ATATATTATG	TCTCATTTTC	TTCAATATGT	ACTTATTTAT	ATTTTACCGT	2200
AATTTACTAT	ATTTAGTTGC	AGAAAGAATT	TTCTCAAAGC	TAGAAGTTTG	2250
CTTCACTATA	AGTATTCAGT	ATAAAGAATA	TTTCGCTATT	ATTTACTTGA	2300
AATGAAAGAC	TGCGGAGGCT	AACTATGTCA	AAAATCATGA	ACCTCATTAC	2350
TTATGATAAG	CTTCTTAAAA	ACATAACAGC	AATTCACATA	AACCTCATAT	2400
GTTCTGATAC	ATTCAAAATC	CCTTTATGAA	GCGGCTGAAA	AAACCGCATC	2450
ATTTATGATA	TGCTTCTCCA	CGCATAATCT	TAAATGCTCT	ATACACTTGC	2500
TCAATTAACA	CAACCCGCAT	CATTTGATGT	GGGAATGTCA	TTTTGCTGAA	2550
TGATAGTGCG	TAGTTACTGC	GTTGTAAGAC	GTCCTTGTGC	AGGCCGTTTG	2600
ATCCGCCAAT	GACGAATACA	AAGTCGCTTT	GCCCTTGGGT	CATGCGTTGG	2650
TTCAATTCTT	GGGCCAATCC	TTCGGAAGAT	AGCATCTTTC	CTTGATTTTC	2700
TAATGTAATG	ACTGTGGATT	GTGGTTTAAAT	TTTGGCTAGT	ATTCGTTGGC	2750
CTTCTTTTTTC	TTTTACTTGC	TCAATTTCTT	TGTCGCTCAT	ATTTTCTGGT	2800
GCTTTTTTCGT	CTGGAACCTC	TATGATGTCT	ATCTTGCTGT	ATGGGCCTAA	2850
ACGTTTTTTCA	TATTCTGCTA	TGGCTTGCTT	CCAATATTTT	TCTTTTAGTT	2900

TCCCTACAGC	TAAAATGGTG	ATTTTCATGT	CGTTTGGTCC	TCCAAATTGT	2950
TATCAACTTT	CCAGTTATCC	ACAAGTTATT	AACTTGTTCA	CACTGTTCCC	3000
TCTTATTATA	CCAATATTTT	TTGCAGTTTT	TGATATTTTC	CTGACATTTA	3050

2) INFORMATION FOR SEQ ID NO: 3

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3183 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: NCTC 8325
- (C) ACCESSION NUMBER: AB014440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3

CTGCAGAGGT	AATTATTCCA	AACAATACCA	TTGATTTCAA	AGGAGAAAGA	50
GATGACGTTA	GAACGCGTGA	AACAAATTTA	GGAAACGCGA	TTGCAGATGC	100
TATGGAAGCG	TATGGCGTTA	AGAATTTCTC	TAAAAAGACT	GACTTTGCCG	150
TGACAAATGG	TGGAGGTATT	CGTGCCTCTA	TCGCAAAAGG	TAAGGTGACA	200
CGCTATGATT	TAATCTCAGT	ATTACCATTT	GGAAATACGA	TTGCGCAAAAT	250
TGATGTAAAA	GGTTCAGACG	TCTGGACGGC	TTTCGAACAT	AGTTTAGGCG	300
CACCAACAAC	ACAAAAGGAC	GGTAAGACAG	TGTTAACAGC	GAATGGCGGT	350
TTACTACATA	TCTCTGATTC	AATCCGTGTT	TACTATGATA	TAAATAAACC	400
GTCTGGCAAA	CGAATTAATG	CTATTCAAAT	TTTAAATAAA	GAGACAGGTA	450
AGTTTGAAAA	TATTGATTTA	AAACGTGTAT	ATCACGTAAC	GATGAATGAC	500
TTACAGCAT	CAGGTGGCGA	CGGATATAGT	ATGTTCCGGT	GTCCTAGAGA	550
AGAAGGTATT	TCATTAGATC	AAGTACTAGC	AAGTTATTTA	AAAACAGCTA	600
ACTTAGCTAA	GTATGATACG	ACAGAACCAC	AACGTATGTT	ATTAGGTAAA	650
CCAGCAGTAA	GTGAACAACC	AGCTAAAGGA	CAACAAGGTA	GCAAAGGTAG	700
TAAGTCTGGT	AAAGATACAC	AACCAATTGG	TGACGACAAA	GTGATGGATC	750
CAGCGAAAAA	ACCAGCTCCA	GGTAAAGTTG	TTTTGTTGCT	AGCGCATAGA	800
GGAAGTGTTA	GTAGCGGTAC	AGAAGGTTCT	GGTCGCACAA	TAGAAGGAGC	850
TACTGTATCA	AGCAAGAGTG	GGAAACAATT	GGCTAGAATG	TCAGTGCCTA	900
AAGGTAGCGC	GCATGAGAAA	CAGTTACCAA	AAACTGGAAC	TAATCAAAGT	950
TCAAGCCCAG	AAGCGATGTT	TGTATTATTA	GCAGGTATAG	GTTTAATCGC	1000
GACTGTACGA	CGTAGAAAAG	CTAGCTAAAA	TATATTGAAA	ATAATACTAC	1050
TGTATTTCTT	AAATAAGAGG	TACGGTAGTG	TTTTTTTTATG	AAAAAAAGCG	1100
ATAACCGTTG	ATAAATATGG	GATATAAAAA	CGAGGATAAG	TAATAAGACA	1150
TCAAGGTGTT	TATCCACAGA	AATGGGGATA	GTTATCCAGA	ATTGTGTACA	1200
ATTTAAAGAG	AAATACCCAC	AATGCCCACA	GAGTTATCCA	CAAATACACA	1250
GGTTATACAC	TAAAAATCGG	GCATAAATGT	CAGGAAAATA	TCAAAAAC TG	1300
CAAAAAATAT	TGGTATAATA	AGAGGGGAACA	GTGTGAACAA	GTTAATAACT	1350
TGTGGATAAC	TGGAAAGTTG	ATAACAATTT	GGAGGACCAA	ACGACATGAA	1400
AATCACCATT	TTAGCTGTAG	GGAAACTAAA	AGAGAAATAT	TGGAAGCAAG	1450

CCATAGCAGA	ATATGAAAAA	CGTTTtagGCC	CATACACCAA	GATAGACATC	1500
ATAGAAgTTC	CAGACGAAAA	AGCACCAGAA	AATATGAGTG	ACAAAGAAAT	1550
TGAGCAAGTA	AAAGAAAAAG	AAGGCCAACG	AATACTAGCC	AAAATCAAAC	1600
CACAATCCAC	AGTCATTACA	TTAGAAATAC	AAGGAAAGAT	GCTATCTTCC	1650
GAAGGATTGG	CCCAAGAATT	GAACCAACGC	ATGACCCAAG	GGCAAAGCGA	1700
CTTTGTTTTT	GTCATTGGCG	GATCAAACGG	CCTGCACAAG	GACGTCTTAC	1750
AACGCAGTAA	CTACGCACTA	TCATTcAGCA	AAATGACATT	CCCACATCAA	1800
ATGATGCGGG	TTGTGTTAAT	TGAACAAGTG	TACAGAGCAT	TTAAGATTAT	1850
GCGAGGAGAG	GCGTATCATA	AGTAAAACTA	AAAAATTCTG	TATGAGGAGA	1900
TAATAATTTG	GAGGGTGTTA	AATGGTGgAC	ATTAAATCCA	CGTTCATTCA	1950
ATATATAAGA	TATATCACGA	TAATTGCGCA	TATAACTTAA	GTAGTAGCTA	2000
ACAGTTGAAA	TTAGGCCCTA	TCAAATTGGT	TTATATCTAA	AATGATTAAAT	2050
ATAGAATGCT	TCTTTTTGTC	CTTATTAAAT	TATAAAAGTA	ACTTTGCAAT	2100
AGAAACAGTT	ATTTcATAAT	CAACAGTCAT	TGACGTAGCT	AAGTAATGAT	2150
AAATAATCAT	AAATAAAATT	ACAGATATTG	ACAAAAAATA	GTAAATATTC	2200
CAATGAAGTT	TCAAAAGAAC	AATTCCAAGA	AATTGAGAAT	GTAAATAATA	2250
AGGTCAAAGA	ATTTTATTAA	GATTTGAAAG	AGTATCAATC	AAGAAAGATG	2300
TAGTTTTTTT	ATAAACTATT	TGGAAAATAA	TTATCATAAT	TTAAAAACTG	2350
ACAATTTGCG	AGACTCATAA	AATGTAATAA	TGGAAATAGA	TGTAAAATAT	2400
AATTAAGGGG	TGTAATATGA	AGATTAATAT	TTATAAATCT	ATTTATAATT	2450
TTCAGGAAAC	AAATACAAAT	TTTTTtagAGA	ATCTAGAATC	TTTAAATGAT	2500
GACAATTATG	AACTGCTTAA	TGATAAAGAA	CTTGTTAGTG	ATTCAAATGA	2550
ATTAAAATTA	ATTAGTAAAG	TTTATATACG	TAAAAAAGAC	AAAAAACTAT	2600
TAGATTGGCA	ATTATTAATA	AAGAATGTAT	ACCTAGATAC	TGAAGAAGAT	2650
GACAATTTAT	TTTCAGAATC	CGGTCATCAT	TTTGATGCAA	TATTATTTCT	2700
CAAAGAAGAT	ACTACATTAC	AAAATAATGT	ATATATTATA	CCTTTTGGAC	2750
AAGCATATCA	TGATATAAAT	AATTTGATTG	ATTATGACTT	CGGAATTGAT	2800
TTTGCAGAAA	GAGCAATCAA	AAATGAAGAC	ATAGTTAATA	AAAATGTTAA	2850
TTTTTTTCAA	CAAAACAGGC	TTAAAGAGAT	TGTTAATTAT	AGAAGGAATA	2900
GTGTAGATTA	CGTTAGACCT	TCAGAATCTT	ATATATCAGT	CCAAGGACAT	2950
CCACAGAATC	CTCAAATTTT	TGGAAAAACA	ATGACTTGtG	GTACAAAGTAT	3000
TTCATTGCGT	GTACCGAATA	GAAAGCAGCA	ATTCATAGAT	AAAATTAGTG	3050
TGATAATCAA	AGAAATAAAC	GCTATTATTA	ATCTTCCTCA	AAAAATTAGT	3100
GAATTTcCTA	GAATAGTAAC	TTTAAAGAGC	TTGAATAAAA	TAGAAGTATT	3150
AGATACTTTA	TTGCTAAAAA	AACTATCGAA	TTC		3183

2) INFORMATION FOR SEQ ID NO: 4

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: 86/560
- (C) ACCESSION NUMBER: AB013471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4

TTCGTCATTG	GCGGATCAAA	CGGCCTGCAC	AAGGACGTCT	TACAACGCAG	50
TAACTACGCA	CTATCATTCA	GCAAAATGAC	ATTCCCACAT	CAAATGATGC	100
GGGTTGTGTT	AATTGAACAA	GTGTACAGAG	CATTTAAGAT	TATGCGTGGA	150
GAAGCGTATC	ATAAATAAAA	CTAAAAATTA	GGTTGTGTAT	AATTTAAAAA	200
TTTAATGAGA	TGTGGAGGAA	TTACATATAT	GAAATATTGG	ATTATACCTT	250
GCAATATCAT	ACGATGTTTA	TAGAGTGTTT	AATAAACCAT	TTTTCAACTA	300
TTGATGATCT	AGAATATATA	ATAACTGTAC	AAATTATATT	GATTATGGAA	350
CTACAATTAA	ATTAAGAAAT	TGATGATGAA	ATTTTAAATT	TAAACTAATG	400
GAATCAAGAA	AGAATGAAAG	GAAATATACA	ATGCCTACGA	TTAATAAAAG	450
GAAGTTTATT	AGATTTTGTG	TTAGAAACA			479

2) INFORMATION FOR SEQ ID NO: 5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: 86/961
- (C) ACCESSION NUMBER: AB013472

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5

TTCGTCATTG	GCGGATCAAA	CGGCCTGCAC	AAGGACGTCT	TACAACGCAG	50
TAACTACGCA	CTATCATTCA	GCAAAATGAC	ATTCCCACAT	CAAATGATGC	100
GGGTTGTGTT	AATTGAACAA	GTGTACAGAG	CATTTAAGAT	TATGCGTGGA	150
GAAGCGTATC	ATAAATAAAA	CTAAAAATTA	GGTTGTGTAT	AATTTAAAAA	200
TTTAATGAGA	TGTGGAGGAA	TTACATATAT	GAAATATTGG	ATTATACCTT	250
GCAATATCAT	ACGATGTTTA	TAGAGTGTTT	AATAAACCAT	TTTTCAACTA	300
TTGATGATCT	AGAATATATA	ATAACTGTAC	AAATTATATT	GATTATGGAA	350
CTACAATTAA	ATTAAGAAAT	TGATGATGAA	ATTTTAAATT	TAAACTAATG	400
GAATCAAGAA	AGAATGAAAG	GAAATATAAC	ATGCCTACGA	TTAATAAAAG	450
GAAGTTTATT	AGATTTTGTG	TTAGAAACAG			480

2) INFORMATION FOR SEQ ID NO: 6

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Staphylococcus aureus

(B) STRAIN: 85/3907

(C) ACCESSION NUMBER: AB013473

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6

TTCGTCATTG	GCGGATCAAA	CGGCCTGCAC	AAGGACGTCT	TACAACGCAG	50
TAACTACGCA	CTATCATTCA	GCAAAATGAC	ATCCCCACAT	CAAATGATGC	100
GGGTTGTGTT	AATTGAACAA	GTGTACAGAG	CATTTAAGAT	TATGCGTGGA	150
GAAGCGTATC	ATAAATAAAA	CTAAAAATTA	GGTTGTGTAT	AATTTAAAAA	200
TTTAATGAGA	TGTGGAGGAA	TTACATATAT	GAAATATTGG	ATTATACCTT	250
GCAATATCAT	ACGATGTTTA	TAGAGTGTTT	AATAAACCAT	TTTTCAACTA	300
TTGATGATCT	AGAATATATA	ATAACTGTAC	AAATTATATT	GATTATGGAA	350
CTACAATTAA	ATTAAGAAAT	TGATGATGAA	ATTTTAAATT	TAAACTAATG	400
GAATCAAGAA	AGAATGAAAG	GAAATATACA	ATGCCTACGA	TTAATAAAAG	450
GAAGTTTATT	AGATTTGTGT	TAGAAACAGT			480

2) INFORMATION FOR SEQ ID NO: 7

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 480 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Staphylococcus aureus

(B) STRAIN: 86/2652

(C) ACCESSION NUMBER: AB013474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7

TTCGTCATTG	GCGGATCAAA	CGGCCTGCAC	AAGGACGTCT	TACAACGCAG	50
TAACTACGCA	CTATCATTCA	GCAAAATGAC	ATCCCCACAT	CAAATGATGC	100
GGGTTGTGTT	AATTGAACAA	GTGTACAGAG	CATTTAAGAT	TATGCGTGGA	150
GAAGCGTATC	ATAAATAAAA	CTAAAAATTA	GGTTGTGTAT	AATTTAAAAA	200
TTTAATGAGA	TGTGGAGGAA	TTACATATAT	GAAATATTGG	ATTATACCTT	250
GCAATATCAT	ACGATGTTTA	TAGAGTGTTT	AATAAACCAT	TTTTCAACTA	300
TTGATGATCT	AGAATATATA	ATAACTGTAC	AAATTATATT	GATTATGGAA	350
CTACAATTAA	ATTAAGAAAT	TGATGATGAA	ATTTTAAATT	TAAACTAATG	400
GAATCAAGAA	AGAATGAAAG	GAAATATACA	ATGCCTACGA	TTAATAAAAG	450
GAAGTTTATT	AGATTTTGTG	TTAGAAACAG			480

2) INFORMATION FOR SEQ ID NO: 8

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: 85/1340
- (C) ACCESSION NUMBER: AB013475

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8

GGCGGATCAA	ACGGCCTGCA	CAAGGACGTC	TTACAACGCA	GTAAC TACGC	50
ACTATCATTC	AGCAAAATGA	CATTCCCACA	TCAAATGATG	CGGGTTGTGT	100
TAATTGAACA	AGTG TACAGA	GCATTTAAGA	TTATGCGTGG	AGAAGCGTAT	150
CATAAATAAA	ACTAAAAATT	AGGTTGTGTA	TAATTTAAAA	ATCTAATGAG	200
ATGTGGAGGA	ATTACATATA	TGAAATATTG	GATTATNCCT	TGCAATATCA	250
TACGATGTTT	ATAGAGTGTT	TAATAAACCA	TTTTTCAACT	ATTGATGATC	300
TACAATATA					309

2) INFORMATION FOR SEQ ID NO: 9

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: 85/1762
- (C) ACCESSION NUMBER: AB013476

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9

TTGGCGGATC	AAACGGCCTG	CACAAGGACG	TCTTACAACG	CAGTAACTAC	50
GCACTATCAT	TCAGCAAAAT	GACATTCCCA	CATCAAATGA	TGCGGGTTGT	100
GTTAATTGAA	CAAGTGTACA	GAGCATTTAA	GATTATGCGT	GGAGAAGCGT	150
ATCATAAATA	AAACTAAAAA	TTAGGTTGTG	TATAATTTAA	AAATTTAATG	200
AGATGTGGAG	GAATTACATA	TATGAAATAT	TGGATTATAC	CTTGCAATAT	250
CATACGATGT	TTATAGAGTG	TTTAATAAAC	CATTTTTCAA	CTATTGATGA	300

TCTAGAATAT	ATAATAACTG	TACAAATTAT	ATTGATTATG	GAACTACAAT	350
TAAATTAAGA	AATTGATGAT	GAAATTTTAA	ATTTAAACTA	ATGGAATCAA	400
GAAAGAATGA	AAGGAAATAT	ACAATGCCTA	CGATTAATAA	AAGGAAGTTT	450
ATTAGATTTT	GTGTTAGAAA	C			471

2) INFORMATION FOR SEQ ID NO: 10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: 85/2082
- (C) ACCESSION NUMBER: AB013477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10

TTCGTCATTG	GCGGATCAAA	CGGCCTGCAC	AAGGACGTCT	TACAACGCAG	50
TAACTACGCA	CTATCATTCA	GCAAAATGAC	ATTCCACAT	CAAATGATGC	100
GGGTTGTGTT	AATTGAACAA	GTGTACAGAG	CATTTAAGAT	TATGCGTGGA	150
GAAGCGTATC	ATAAATAAAA	CTAAAAATTA	GGTTGTGTAT	AATTTAAAAA	200
TTTAATGAGA	TGTGGAGGAA	TTACATATAT	GAAATATTGG	ATTATACCTT	250
GCAATATCAT	ACGATGTTTA	TAGAGTGTTT	AATAAAACCAT	TTTTCAACTA	300
TTGATGATCT	AGAATATATA	ATAACTGTAC	AAATTATATT	GATTATGGAA	350
CTACAATTAA	ATTAAGAAAT	TGATGATGAA	ATTTTAAATT	TAAACTAATG	400
GAATCAAGAA	AGAATGAAAG	GAAATATACA	ATGCCTACGA	TTAATAAAAG	450
GAAGTTTATT	AGATTTTGTG	TTAGAAACAG			480

2) INFORMATION FOR SEQ ID NO: 11

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: 85/2111
- (C) ACCESSION NUMBER: AB013478

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11

TTCGTCATTG	GCGGATCAAA	CGGCCTGCAC	AAGGACGTCT	TACAACGCAG	50
TAACTACGCA	CTATCATTCA	GCAAAATGAC	ATCCCCACAT	CAAATGATGC	100
GGGTTGTGTT	AATTGAACAA	GTGTACAGAG	CATTTAAGAT	TATGCGTGGA	150
GAAGCGTATC	ATAAATAAAA	CTAAAAATTA	GGTTGTGTAT	AATTTAAAAA	200
TTTAATGAGA	TGTGGAGGAA	TTACATATAT	GAAATATTGG	ATTATACCTT	250
GCAATATCAT	ACGATGTTTA	TAGAGTGTTT	AATAAACCAT	TTTTCAACTA	300
TTGATGATCT	AGAATATATA	ATAACTGTAC	AAATTATATT	GATTATGGAA	350
CTACAATTAA	ATTAAGAAAT	TGATGATGAA	ATTTTAAATT	TAAACTAATG	400
GAATCAAGAA	AGAATGAAAG	GAAATATACA	ATGCCTACGA	TTAATAAAAG	450
GAAGTTTATT	AGATTTTGTG	TTAGAAACAG			480

2) INFORMATION FOR SEQ ID NO: 12

- (i) (A) LENGTH: 480 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: 85/5495
- (C) ACCESSION NUMBER: AB013479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12

TTCGTCATTG	GCGGATCAAA	CGGCCTGCAC	AAGGACGTCT	TACAACGCAG	50
TAACTACGCA	CTATCATTCA	GCAAAATGAC	ATCCCCACAT	CAAATGATGC	100
GGGTTGTGTT	AATTGAACAA	GTGTACAGAG	CATTTAAGAT	TATGCGTGGA	150
GAAGCGTATC	ATAAATAAAA	CTAAAAATTA	GGTTGTGTAT	AATTTAAAAA	200
TTTAATGAGA	TGTGGAGGAA	TTACATATAT	GAAATATTGG	ATTATACCTT	250
GCAATATCAT	ACGATGTTTA	TAGAGTGTTT	AATAAACCAT	TTTTCAACTA	300
TTGATGATCT	AGAATATATA	ATAACTGTAC	AAATTATATT	GATTATGGAA	350
CTACAATTAA	ATTAAGAAAT	TGATGATGAA	ATTTTAAATT	TAAACTAATG	400
GAATCAAGAA	AGAATGAAAG	GAAATATACA	ATGCCTACGA	TTAATAAAAG	450
GAAGTTTATT	AGATTTTGTG	TTAGAAACAG			480

2) INFORMATION FOR SEQ ID NO: 13

- (i) (A) LENGTH: 478 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
 (B) STRAIN: 85/1836
 (C) ACCESSION NUMBER: AB013480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13

TTCGTCATTG	GCGGATCAAA	CGGCCTGCAC	AAGGACGTCT	TACAACGCAG	50
TAACTACGCA	CTATCATTCA	GCAAAATGAC	ATTCCCACAT	CAAATGATGC	100
GGGTTGTGTT	AATTGAACAA	GTGTACAGAG	CATTTAAGAT	TATGCGTGGA	150
GAAGCGTATC	ATAAATAAAA	CTAAAAATTA	GGTTGTGTAT	AATTTAAAAA	200
TTTAATGAGA	TGTGGAGGAA	TTACATATAT	GAAATATTGG	ATTATACCTT	250
GCAATATCAT	ACGATGTTTA	TAGAGTGTTT	AATAAACCAT	TTTTCAACTA	300
TTGATGATCT	AGAATATATA	ATAACTGTAC	AAATTATATT	GATTATGGAA	350
CTACAATTAA	ATTAAGAAAT	TGATGATGAA	ATTTTAAATT	TAAACTAATG	400
GAATCAAGAA	AGAATGAAAG	GAAATATACA	ATGCCTACGA	TTAATAAAAG	450
GAAGTTTATT	AGATTTTGTG	TTAGAAAC			478

2) INFORMATION FOR SEQ ID NO: 14.

- (i) (A) LENGTH: 479 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
 (B) STRAIN: 85/2147
 (C) ACCESSION NUMBER: AB013481

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14

TTCGTCATTG	GCGGATCAAA	CGGCCTGCAC	AAGGACGTCT	TACAACGCAG	50
TAACTACGCA	CTATCATTCA	GCAAAATGAC	ATTCCCACAT	CAAATGATGC	100
GGGTTGTGTT	AATTGAACAA	GTGTACAGAG	CATTTAAGAT	TATGCGTGGA	150
GAAGCGTATC	ATAAATAAAA	CTAAAAATTA	GGTTGTGTAT	AATTTAAAAA	200
TTTAATGAGA	TGTGGAGGAA	TTACATATAT	GAAATATTGG	ATTATACCTT	250
GCAATATCAT	ACGATGTTTA	TAGAGTGTTT	AATAAACCAT	TTTTCAACTA	300
TTGATGATCT	AGAATATATA	ATAACTGTAC	AAATTATATT	GATTATGGAA	350
CTACAATTAA	ATTAAGAAAT	TGATGATGAA	ATTTTAAATT	TAAACTAATG	400
GAATCAAGAA	AGAATGAAAG	GAAATATACA	ATGCCTACGA	TTAATAAAAG	450
GAAGTTTATT	AGATTTTGTG	TTAGAAACA			479

2) INFORMATION FOR SEQ ID NO: 15

- (i) (A) LENGTH: 480 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: 85/3619
- (C) ACCESSION NUMBER: AB013482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15

TTCGTCATTG	GCGGATCAAA	CGGCCTGCAC	AAGGACGTCT	TACAACGCAG	50
TAACTACGCA	CTATCATTCA	GCAAAATGAC	ATTCCCACAT	CAAATGATGC	100
GGGTTGTGTT	AATTGAACAA	GTGTACAGAG	CATTTAAGAT	TATGCGTGGA	150
GAAGCGTATC	ATAAATAAAA	CTAAAAATTA	GGTTGTGTAT	AATTTAAAAA	200
TTTAATGAGA	TGTGGAGGAA	TTACATATAT	GAAATATTGG	ATTATACCTT	250
GCAATATCAT	ACGATGTTTA	TAGAGTGTTT	AATAAACCAT	TTTTCAACTA	300
TTGATGATCT	AGAATATATA	ATAACTGTAC	AAATTATATT	GATTATGGAA	350
CTACAATTAA	ATTAAGAAAT	TGATGATGAA	ATTTTAAATT	TAAACTAATG	400
GAATCNCGAA	AGAATGAAAG	GAAATATACA	ATGCCTACGA	TTAATAAAAG	450
GAAGTTTATT	AGATTTTGTG	TTAGAAACAG			480

2) INFORMATION FOR SEQ ID NO: 16

- (i) (A) LENGTH: 480 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: 85/3566
- (C) ACCESSION NUMBER: AB013483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16

TTCGTCATTG	GCGGATCAAA	CGGCCTGCAC	AAGGACGTCT	TACAACGCAG	50
TAACTACGCA	CTATCATTCA	GCAAAATGAC	ATTCCCACAT	CAAATGATGC	100
GGGTTGTGTT	AATTGAACAA	GTGTACAGAG	CATTTAAGAT	TATGCGTGGA	150
GAAGCGTATC	ATAAATAAAA	CTAAAAATTA	GGTTGTGTAT	AATTTAAAAA	200
TTTAATGAGA	TGTGGAGGAA	TTACATATAT	GAAATATTGG	ATTATACCTT	250
GCAATATCAT	ACGATGTTTA	TAGAGTGTTT	AATAAACCAT	TTTTCAACTA	300
TTGATGATCT	AGAATATATA	ATAACTGTAC	AAATTATATT	GATTATGGAA	350
CTACAATTAA	ATTAAGAAAT	TGATGATGAA	ATTTTAAATT	TAAACTAATG	400
GAATCAAGAA	AGAATGAAAG	GAAATATACA	ATGCCTACGA	TTAATAAAAG	450

GAAGTTTATT AGATTTTGTG TTAGAAACAG

480

2) INFORMATION FOR SEQ ID NO: 17

- (i) (A) LENGTH: 480 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: 85/2232
- (C) ACCESSION NUMBER: AB014402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17

TTCGTCATTG	GCGGATCAAA	CGGCCTGCAC	AAGGACGTCT	TACAACGCAG	50
TAACTACGCA	CTATCATTTCA	GCAAAATGAC	ATCCCCACAT	CAAATGATGC	100
GGGTTGTGTT	AATTGAACAA	GTGTACAGAG	CATTTAAGAT	TATGCGTGGA	150
GAAGCATATC	ATAAATGATG	CGGTTTTTTC	AGCCGCTTCA	TAAAGGGATT	200
TTGAATGTAT	CAGAACATAT	GAGGTTTATG	TGAATTGCTG	TTATGTTTTT	250
AAGAAGCTTA	TCATAAGTAA	TGAGGTTTCAT	GATTTTTTGAC	ATAGTTAGCC	300
TCCGCAGTCT	TTCATTTCAA	GTAAATAATA	GCGAAATATT	CTTTTACTG	350
AATACTTATA	GTGAAGCAAA	GTTCTAGCTT	TGAGAAAATT	CTTTCTGCAA	400
CTAAATATAG	TAAATTACGG	TAAATATATA	ATAAGTACAT	ATTGAAGAAA	450
ATGAGACATA	ATATATTTTA	TAATAGGAGG			480

2) INFORMATION FOR SEQ ID NO: 18

- (i) (A) LENGTH: 480 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: 85/2235
- (C) ACCESSION NUMBER: AB014403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18

TTCGTCATTG	GCGGATCAAA	CGGCCTGCAC	AAGGACGTCT	TACAACGCAG	50
TAACTACGCA	CTATCATTTCA	GCAAAATGAC	ATCCCCACAT	CAAATGATGC	100
GGGTTGTGTT	AATTGAGCAA	GTGTATAGAG	CATTTAAGAT	TATGCGTGGA	150

GAAGCATATC	ATAAATGATG	CGGTTTTTTC	AGCCGCTTCA	TAAAGGGATT	200
TTGAATGTAT	CAGAACATAT	GAGGTTTATG	TGAATTGCTG	TTATGTTTTT	250
AAGAAGCTTA	TCATAAGTAA	TGAGGTTTCAT	GATTTTTTGAC	ATAGTTAGCC	300
TCCGCAGTCT	TTCATTTCAA	GTAAATAATA	GCGAAATATT	CTTTATACTG	350
AATACTTATA	GTGAAGCAAA	GTTCTAGCTT	TGAGAAAATT	CTTTCTGCAA	400
CTAAATATAG	TAAATTACGG	TAAATATAAA	ATAAGTACAT	ATTGAAGAAA	450
ATGAGACATA	ATATATTTTA	TAATAGGAGG			480

2) INFORMATION FOR SEQ ID NO: 19

- (i) (A) LENGTH: 458 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: MR108
- (C) ACCESSION NUMBER: AB014404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19

TTCGTCATTG	GCGGATCAAA	CGGCCTGCAC	AAGGACGTCT	TACAACGCAG	50
TAACTACGCA	CTATCATTC	GCAAAATGAC	ATCCCCACAT	CAAATGATGC	100
GGGTTGTGTT	AATTGAACAA	GTGTACAGAG	CATTTAAGAT	TATGCGTGGA	150
GAAGCATATC	ATAAATGATG	CGGTTTTTTC	AGCCGCTTCA	TAAAGGGATT	200
TTGAATGTAT	CAGAACATAT	GAGGTTTATG	TGAATTGCTG	TTATGTTTTT	250
AAGAAGCTTA	TCATAAGTAA	TGAGGTTTCAT	GATTTTTTGAC	ATAGTTAGCC	300
TCCGCAGTCT	TTCATTTCAA	GTAAATAATA	GCGAAATATT	CTTTATACTG	350
AATACTTATA	GTGAAGCAAA	GTTCTAGCTT	TGAGAAAATT	CTTTCTGCAA	400
CTAAATATAG	TAAATTACGG	TAAATATAAA	ATAAGTACAT	ATTGAAGAAA	450
ATGAGACA					458

2) INFORMATION FOR SEQ ID NO: 20

- (i) (A) LENGTH: 385 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: 85/9302
- (C) ACCESSION NUMBER: AB014430

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20

TTCGTCATTG	GCGGATCAAA	CGGCCTGCAC	AAGGACGTCT	TACAACGCAG	50
TAACTACGCA	CTATCATTCA	GCAAAATGAC	ATTCCCACAT	CAAATGATGC	100
GGGTTGTGTT	AATTGAGCAA	GTGTATAGAG	CATTTAAGAT	TATGCGTGGA	150
GAAGCTTATC	ATAAGTAATG	AGGTTCATGA	TTTTTGACAT	AGTTAGCCTC	200
CGCAGTCTTT	CATTTCAAGT	AAATAATAGC	GAAATATTCT	TTATACTGAA	250
TACTTATAGT	GAAGCAAAGT	TCTAGCTTTG	AGAAAATTCT	TTCTGCAACT	300
AAATATAGTA	AATTACGGTA	AAATATAAAT	AAGTACATAT	TGAAGAAAAT	350
GAGACATAAT	ATATTTTATA	ATAGGAGGGA	ATTTTC		385

2) INFORMATION FOR SEQ ID NO: 21

- (i) (A) LENGTH: 385 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: 84/9580
- (C) ACCESSION NUMBER: AB014431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21

TTCGTCATTG	GCGGATCAAA	CGGCCTGCAC	AAGGACGTCT	TACAACGCAG	50
TAACTACGCA	CTATCATTCA	GCAAAATGAC	ATTCCCACAT	CAAATGATGC	100
GGGTTGTGTT	AATTGAGCAA	GTGTATAGAG	CATTTAAGAT	TATGCGTGGA	150
GAAGCTTATC	ATAAGTAATG	AGGTTCATGA	TTTTTGACAT	AGTTAGCCTC	200
CGCAGTCTTT	CATTTCAAGT	AAATAATAGC	GAAATATTCT	TTATACTGAA	250
TACTTATAGT	GAAGCAAAGT	TCTAGCTTTG	AGAAAATTCT	TTCTGCAACT	300
AAATATAGTA	AATTACGGTA	AAATATAAAT	AAGTACATAT	TGAAGAAAAT	350
GAGACATAAT	ATATTTTATA	ATAGGAGGGA	ATTTTC		385

2) INFORMATION FOR SEQ ID NO: 22

- (i) (A) LENGTH: 385 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus

(B) STRAIN: 85/1940
 (C) ACCESSION NUMBER: AB014432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22

TTCGTCATTG	GCGGATCAAA	CGGCCTGCAC	AAGGACGTCT	TACAACGCAG	50
TAAGTACGCA	CTATCATTCA	GCAAAATGAC	ATTCCCACAT	CAAATGATGC	100
GGGTTGTGTT	AATTGAGCAA	GTGTATAGAG	CATTTAAGAT	TATGCGTGGA	150
GAAGCTTATC	ATAAGTAATG	AGGTTTCATGA	TTTTTGACAT	AGTTAGCCTC	200
CGCAGTCTTT	CATTTCAAGT	AAATAATAGC	GAAATATTCT	TTATACTGAA	250
TACTTATAGT	GAAGCAAAGT	TCTAGCTTTG	AGAAAATTCT	TTCTGCAACT	300
AAATATAGTA	AATTACGGTA	AAATATAAAT	AAGTACATAT	TGAAGAAAAT	350
GAGACATAAT	ATATTTTATA	ATAGGAGGGA	ATTTTC		385

2) INFORMATION FOR SEQ ID NO: 23

(i) (A) LENGTH: 385 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Staphylococcus aureus
 (B) STRAIN: 61/6219
 (C) ACCESSION NUMBER: AB014433

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23

TTCGTCATTG	GCGGATCAAA	CGGCCTGCAC	AAGGACGTCT	TACAACGCAG	50
TAAGTACGCG	CTATCATTCA	GCAAAATGAC	ATTCCCACAT	CAAATGATGC	100
GGGTTGTGTT	AATTGAACAA	GTGTACAAAG	CATTTAAGAT	TATGCGAGGA	150
GAAGCTTATC	ATAAGTAATG	AGGTTTCATGA	TTTTTGACAT	AGTTAGCCTC	200
CGCAGTCTTT	CATTTCAAGT	AAATAATAGC	GAAATATTCT	TTATACTGAA	250
TACTTATAGT	GAAGCAAAGT	TCTAGCTTTG	AGAAAATTCT	TTCTGCAACT	300
AAATATAGTA	AATTACGGTA	AAATATAAAT	AAGTACATAT	TGAAGAAAAT	350
GAGACATAAT	ATATTTTATA	ATAGGAGGGA	ATTTTC		385

2) INFORMATION FOR SEQ ID NO: 24

(i) (A) LENGTH: 340 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: 64/4176
- (C) ACCESSION NUMBER: AB014434

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24

CGCAGTAACT	ACGCGCTATC	ATTCAGCAAA	ATGACATTCC	CACATCAAAT	50
GATGCGGGTT	GTGTTAGTTG	AGCAAGTGTA	CATAGCATTT	AAGATTATGC	100
GAGGAGAAGC	TTATCATAAG	TAATGAGGTT	CATGATTTTT	GACATAGTTA	150
GCCTCCGCAG	TCTTTCATTT	CAAGTAAATA	ATAGCGAAAT	ATTCTTTATA	200
CTGAATACTT	ATAGTGAAGC	AAAGTTCTAG	CTTTGAGAAA	ATTCTTTCTG	250
CAACTAAATA	TAGTAAATTA	CGGTAAAATA	TAAATAAGTA	CATATTGAAG	300
AAAATGAGAC	ATAATATATT	TTATAATAGG	AGGGAATTC		340

2) INFORMATION FOR SEQ ID NO: 25

- (i) (A) LENGTH: 369 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: 64/3846
- (C) ACCESSION NUMBER: AB014435

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25

CAAACGGCCT	GCACAAGGAC	GTCTTACAAC	GCAGTAACTA	CGCACTATCA	50
TTCAGCAAAA	TGACATTCCC	ACATCAAATG	ATGCGGGTTG	TGTTAATTGA	100
ACAAGTGTAC	AGAGCATTTA	AGATTATGCG	AGGAGAAGCT	TATCATAAGT	150
AATGAGGTTT	ATGATTTTTG	ACATAGTTAG	CCTCCGCAGT	CTTTCATTTT	200
AAGTAAATAA	TAGCGAAATA	TTCTTTATAC	TGAATACTTA	TAGTGAAGCA	250
AAGTTCTAGC	TTTGAGAAAA	TTCTTTCTGC	AACTAAATAT	AGTAAATTAC	300
GGTAAAATAT	AAATAAGTAC	ATATTGAAGA	AAATGAGACA	TAATATATTT	350
TATAATAGGA	GGGAATTC				369

2) INFORMATION FOR SEQ ID NO: 26

- (i) (A) LENGTH: 3050 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: HUC19
 (C) ACCESSION NUMBER: Extracted from AF181950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26

AATTTGGTAA	ACCTCAAAAG	GTAATTACAG	ATCAGGCACC	TTCAACGAAG	50
GTAGCAATGG	CTAAAGTAAT	TAAAGCTTTT	AAACTTAAAC	CTGACTGTCA	100
TTGTACATCG	AAATATCTGA	ATAACCTCAT	TGAGCAAGAT	CACCGTCATA	150
TTAAAGTAAG	AAAGACAAGG	TATCAAAGTA	TCAATACAGC	AAAGAATACT	200
TTAAAAGGTA	TTGAATGTAT	TCACGCTCTA	TATAAAAAGA	ACCGCAGGTC	250
TCTTCAGATC	TACGGATTTT	CGCCATGCCA	CGAAATTAGC	ATCATGCTAG	300
CAAGTTAAGC	GAACACTGAC	ATGATAAATT	AGTGGTTAGC	TATATTTTTT	350
TACTTTGCAA	CAGAACCGAA	AATAATCTCT	TCAATTTATT	TTTATATGAA	400
TCCTGTGACT	CAATGATTGT	AATATCTAAA	GATTTCAGTT	CATCATAGAC	450
AATGTTCTTT	TCAACATTTT	TTATAGCAAA	TTGATTAAAT	AAATTCTCTA	500
ATTTCTCCCG	TTTGATTTCA	CTACCATAGA	TTATATTATC	ATTGATATAG	550
TCAATGAATA	ATGACAAATT	ATCACTCATA	ACAGTCCCAA	CCCCTTTATT	600
TTGATAGACT	AATTATCTTC	ATCATTGTAA	AACAAATTAC	ACCCTTTAAA	650
TTTAACTCAA	CTTAAATATC	GACAAATTAA	AAAACAATAA	AATTACTTGA	700
ATATTATTCA	TAATATATTA	ACAACTTTAT	TATACTGCTC	TTTATATATA	750
AAATCATTA	TAATTAAACA	AGCCTTAAAA	TATTTAACTT	TTTTGTGATT	800
ATTACACATT	ATCTTATCTG	CTCTTTATCA	CCATAAAAAT	AGAAAAAACA	850
AGATTCCCTAA	AGAATATAGG	AATCTTGTTT	CAGACTGTGG	ACAAACTGAT	900
TTTTTTATCAG	TTAGCTTATT	TAGAAAGTTT	TATTTAAATT	ACAGTTTCTA	950
TTTTTTATTAG	ATCACAATTT	TATTTTAGCT	CTTGTTCAAG	TAATCATTTT	1000
TCGCCAAAAA	CTTTATACTG	AATAGCTTCT	ACATTAAATA	CTTGTCAATG	1050
AGATCATCTA	CATCTTTAAA	TTCAGAATAA	TTCGCATATG	GATCTATAAA	1100
ATAAAATTGT	GGTTCCTTAC	CGGAAACATT	AAATATTCTT	AATATTAAAT	1150
ATTTCTGCTT	ATATTCTTTC	ATAGCAAACA	TTTCATTTAG	CGACATAAAA	1200
AATGGTTCCT	CAATACTAGA	AGATGTAGAT	GTTTAAATTT	CAATAAATTT	1250
TTCTACAGCT	TTATCTGTAT	TTGTTGGATC	AAAAGCTACT	AAATCATAGC	1300
CATGACCGTG	TTGAGAGCCT	GGATTATCAT	TTAAAATATT	CCTAAACTGT	1350
TCTTTCTTAT	CTTCGTCTAT	TTTATTATCA	ATTAGCTCAT	TAAAGTAATT	1400
TAGCGCTAAT	TTTTCTCCAA	CTTTACCGGT	TAATTTATTC	TCTTTATTTG	1450
ATTTTTCAAT	TTCTGAATCA	TTTTTAGTAG	TCTTTGATAC	ACCTTTTTTA	1500
TATTTTGGA	TTATTCCTTT	AGGTGCTTCC	ACTTCCTTGA	GTGTCTTATC	1550
TTTTTGTGCT	GTTCTAATTT	CTTCAATTTT	GCTGTCTTCC	TGTATTTCTG	1600
CTATGCTATT	GACCAAGCTA	TCATAGGATG	TTTTTGTAAC	TTTTGAAGCT	1650
AATTCATTAA	ATAGTTCTAA	AAATTTCTTT	AAATCCTCTA	GCATATCTTC	1700
TTCTGTGAAT	CCTTCATTCA	AATCATAATA	TTTGAATCTT	ATTGATCCAT	1750
GAGAAATATCC	TGATGGATAA	TCATTTTTTA	AATCATAAGA	TGAATCTTTA	1800
TTTTCTGCGT	AATAAAATCT	TCCAGTATTA	AATTCATTTG	ATGTAATATA	1850
TTTATTGAGT	TCGGAAGATA	AAGTTAATGC	TCTTTGTTTT	GCAGCATTTT	1900
TATCCCGCGG	AAACATATCA	CTTATCTTTG	ACCATCCTTG	ATTCAAAGAT	1950
AAGTATATGC	CTTCTCCTTC	CGGATGAAAA	AGATATACCA	AATAATGTCC	2000
ATCCTTTGTT	TCTTTTGTTA	TATTCTCATC	ATATATTGAA	ATCCAAGGAA	2050
CTTTACTATA	GTTCCAGTA	GCAACCTTCC	CTACAACTGA	ATATTTATCT	2100
TCTTTTATAT	GCACTTTTAA	CTGCTTGGGT	AACTTATCAT	GGACTAAAGT	2150
TTTATATAGA	TCACCTTTAT	CCCAATCAGA	TTTTTTAACT	ACATTATTGG	2200

TACGTTTCTC	TTTAATTAAT	TTAAGGACCT	GCATAAAGTT	GTCTATCATT	2250
TGAAATTCCC	TCCTATTATA	AAATATATTA	TGTCTCATTT	TCTTCAATAT	2300
GTACTTATTT	ATATTTTACC	GTAATTTACT	ATATTTAGTT	GCAGAAAGAA	2350
TTTTCTCAAA	GCTAGAACTT	TGCTTCACTA	TAAGTATTCA	GTATAAAGAA	2400
TATTTTCGCTA	TTATTTTACTT	GAAATGAAAG	ACTGCGGAGG	CTAACTATGT	2450
CAAAAATCAT	GAACCTCATT	ACTTATGATA	AGCTTCTTAA	AAACATAACA	2500
GCAATTCACA	TAAACCTCAT	ATGTTCTGAT	ACATTCAAAA	TCCCTTTATG	2550
AAGCGGCTGA	AAAAACCGCA	TCATTTATGA	TATGCTTCTC	CTCGCATAAT	2600
CTTAAATGCT	CTGTACACTT	GTTCAATTAA	CACAACCCGC	ATCATTTGAT	2650
GTGGGAATGT	CATTTTGCTG	AATGATAGTG	CGTAGTTACT	GCGTTGTAAAG	2700
ACGTCCTTGT	GCAGGCCGTT	TGATCCGCCA	ATGACGAAAA	CAAAGTCGCT	2750
TTGCCCTTGG	GTCATGCGTT	GGTTCAATTC	TTGGGCCAAT	CCTTCGGAAG	2800
ATAGCATCTT	TCCTTGTAAT	TCTAATGTAA	TGACTGTGGA	TTGTGGTTTG	2850
ATTTTGGCTA	GTATTCGTTG	GCCTTCTTTT	TCTTTTACTT	GCTCAATTTT	2900
TTTGTCACTC	ATATTTTCTG	GTGCTTTTTC	GTCTGGAAC	TCTATGATGT	2950
CTATCTTGGT	GTATGGGCCT	AAACGTTTTT	CATATTCTGC	TATGGCTTGC	3000
TTCCAATATT	TCTCTTTTAG	TTTCCCTACA	GCTAAATGG	TGATTTTCAT	3050

2) INFORMATION FOR SEQ ID NO: 27

- (i) (A) LENGTH: 657 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: CCRI-2025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27

CCACCTTCAT	ATGACGTCTA	TCCATTTATG	TATGGCATGA	GTAACGAAGA	50
ATATAATAAA	TTAACC GAAG	ATAAAAAAGA	ACCTCTGCTC	AACAAGTTCC	100
AGATTACAAC	TTCACCAGGT	TCAACTCAAA	AAATATTAAC	AGCAATGATT	150
GGGTTAAATA	ACAAAACATT	AGACGATAAA	ACAAGTTATA	AAATCGATGG	200
TAAAGGTTGG	CAAAAAGATA	AATCTTGGGG	TGGTTACAAC	GTTACAAGAT	250
ATGAAGTGGT	AAATGGTAAT	ATCGACTTAA	AACAAGCAAT	AGAATCATCA	300
GATAACATTT	TCTTTGCTAG	AGTAGCACTC	GAATTAGGCA	GTAAGAAATT	350
TGAAAAAGGC	ATGAAAAAAC	TAGGTGTTGG	TGAAGATATA	CCAAGTGATT	400
ATCCATTTTA	TAATGCTCAA	ATTTCAAACA	AAAATTTAGA	TAATGAAATA	450
TTATTAGCTG	ATTAGGTTA	CGGACAAGGT	GAAATACTGA	TTAACCCAGT	500
ACAGATCCTT	TCAATCTATA	GCGCATTAGA	AAATAATGGC	AATATTAACG	550
CACCTCACTT	ATTAAAAGAC	ACGAAAAACA	AAGTTTGGA	GAAAAATATT	600
ATTTCCAAAG	AAAATATCAA	TCTATTAACT	GATGGTATGC	AACAAGTCGT	650
AAATAAA					657

2) INFORMATION FOR SEQ ID NO: 28

- (i) (A) LENGTH: 782 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-1263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28

CACCTTCATA	TGACGTCTAT	CCATTTATGT	ATGGCATGAG	TAACGAAGAA	50
TATAATAAAT	TAACCGAAGA	TAAAAAAGAA	CCTCTGCTCA	ACAAGTTCCA	100
GATTACAAC	TCACCAGGTT	CAACTCAAAA	AATATTAACA	GCAATGATTG	150
GGTTAAATAA	CAAAACATTA	GACGATAAAA	CAAGTTATAA	AATCGATGGT	200
AAAGGTTGGC	AAAAAGATAA	ATCTTGGGGT	GGTTACAACG	TTACAAGATA	250
TGAAGTGGTA	AATGGTAATA	TCGACTTAAA	ACAAGCAATA	GAATCATCAG	300
ATAACATTTT	CTTTGCTAGA	GTAGCACTCG	AATTAGGCAG	TAAGAAATTT	350
GAAAAAGGCA	TGAAAAAACT	AGGTGTTGGT	GAAGATATAC	CAAGTGATTA	400
TCCATTTTAT	AATGCTCAAA	TTTCAAACAA	AAATTTAGAT	AATGAAATAT	450
TATTAGCTGA	TTCAGGTTAC	GGACAAGGTG	AAATACTGAT	TAACCCAGTA	500
CAGATCCTTT	CAATCTATAG	CGCATTAGAA	AATAATGGCA	ATATTAACGC	550
ACCTCACTTA	TTAAAAGACA	CGAAAAACAA	AGTTTGGAAG	AAAAATATTA	600
TTTCCAAAGA	AAATATCAAT	CTATTAAGTG	ATGGTATGCA	ACAAGTCGTA	650
AATAAAACAC	ATAAAGAAGA	TATTTATAGA	TCTTATGCAA	ACTTAATTGG	700
CAAATCCGGT	ACTGCAGAAC	TCAAAATGAA	ACAAGGAGAA	ACTGGCAGAC	750
AAATTGGGTG	GTTTATATCA	TATGATAAAG	AT		782

2) INFORMATION FOR SEQ ID NO: 29

- (i) (A) LENGTH: 744 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-1311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29

TATGACGTCT	ATCCATTTAT	GTATGGCATG	AGTAACGAAG	AATATAATAA	50
ATTAACCGAA	GATAAAAAAG	AACCTCTGCT	CAACAAGTTC	CAGATTACAA	100
CTTCACCAGG	TTCAACTCAA	AAAATATTAA	CAGCAATGAT	TGGGTTAAAT	150
AACAAAACAT	TAGACGATAA	AACAAGTTAT	AAAATCGATG	GTAAAGGTTG	200
GCAAAAAGAT	AAATCTTGGG	GTGGTTACAA	CGTTACAAGA	TATGAAGTGG	250
TAAATGGTAA	TATCGACTTA	AAACAAGCAA	TAGAATCATC	AGATAACATT	300
TTCTTTGCTA	GAGTAGCACT	CGAATTAGGC	AGTAAGAAAT	TTGAAAAAGG	350
CATGAAAAAA	CTAGGTGTTG	GTGAAGATAT	ACCAAGTGAT	TATCCATTTT	400

ATAATGCTCA	AATTTCAAAC	AAAAATTTAG	ATAATGAAAT	ATTATTAGCT	450
GATTTCAGGTT	ACGGACAAGG	TGAAATACTG	ATTAACCCAG	TACAGATCCT	500
TTCAATCTAT	AGCGCATTAG	AAAATAATGG	CAATATTAAC	GCACCTCACT	550
TATTAAAAGA	CACGAAAAAC	AAAGTTTGGG	AGAAAAATAT	TATTTCCAAA	600
GAAAAATATCA	ATCTATTAAC	TGATGGTATG	CAACAAGTCG	TAAATAAAAC	650
ACATAAAGAA	GATATTTATA	GATCTTATGC	AAACTTAATT	GGCAAATCCG	700
GTAATGCAGA	ACTCAAAATG	AAACAAGGAG	AAACTGGCAG	ACAA	744

2) INFORMATION FOR SEQ ID NO: 30

- (i) (A) LENGTH: 652 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: CCRI-1331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30

CCACCTTCAT	ATGACGTCTA	TCCATTTATG	TATGGCATGA	GTAACGAAGA	50
ATATAATAAA	TTAACCGAAG	ATAAAAAAGA	ACCTCTGCTC	AACAAGTTCC	100
AGATTACAAC	TTCACCAGGT	TCAACTCAA	AAATATTAAC	AGCAATGATT	150
GGGTAAATA	ACAAAACATT	AGACGATAAA	ACAAGTTATA	AAATCGATGG	200
TAAAGGTTGG	CAAAAAGATA	AATCTTGGGG	TGGTTACAAC	GTTACAAGAT	250
ATGAAGTGGT	AAATGGTAAT	ATCGACTTAA	AACAAGCAAT	AGAATCATCA	300
GATAACATTT	TCTTTGCTAG	AGTAGCACTC	GAATTAGGCA	GTAAGAAATT	350
TGAAAAAGGC	ATGAAAAAAC	TAGGTGTTGG	TGAAGATATA	CCAAGTGATT	400
ATCCATTTTA	TAATGCTCAA	ATTTCAAACA	AAAATTTAGA	TAATGAAATA	450
TTATTAGCTG	ATTCAGGTTA	CGGACAAGGT	GAAATACTGA	TTAACCCAGT	500
ACAGATCCTT	TCAATCTATA	GCGCATTAGA	AAATAATGGC	AATATTAACG	550
CACCTCACTT	ATTAAAAGAC	ACGAAAAACA	AAGTTTGGAA	GAAAAATATT	600
ATTTCCAAAG	AAAATATCAA	TCTATTAACT	GATGGTATGC	AACAAGTCGT	650
AA					652

2) INFORMATION FOR SEQ ID NO: 31

- (i) (A) LENGTH: 2436 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: CCRI-1377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31

CCACCTTCAT	ATGACGTCTA	TCCATTTATG	TATGGCATGA	GTAACGAAGA	50
ATATAATAAA	TTAACCGAAG	ATAAAAAAGA	ACCTCTGCTC	AACAAGTTCC	100
AGATTACAAC	TTCACCAGGT	TCAACTCAAA	AAATATTAAC	AGCAATGATT	150
GGGTAAATA	ACAAAACATT	AGACGATAAA	ACAAGTTATA	AAATCGATGG	200
TAAAGGTTGG	CAAAAAGATA	AATCTTGGGG	TGGTTACAAC	GTTACAAGAT	250
ATGAAGTGGT	AAATGGTAAT	ATCGACTTAA	AACAAGCAAT	AGAATCATCA	300
GATAACATTT	TCTTTGCTAG	AGTAGCACTC	GAATTAGGCA	GTAAGAAATT	350
TGAAAAAGGC	ATGAAAAAAC	TAGGTGTTGG	TGAAGATATA	CCAAGTGATT	400
ATCCATTTTA	TAATGCTCAA	ATTTCAAACA	AAAATTTAGA	TAATGAAATA	450
TTATTAGCTG	ATTCAGGTTA	CGGACAAGGT	GAAATACTGA	TTAACCCAGT	500
ACAGATCCTT	TCAATCTATA	GCGCATTAGA	AAATAATGGC	AATATTAACG	550
CACCTCACTT	ATTAAAAGAC	ACGAAAAACA	AAGTTTGGAA	GAAAAATATT	600
ATTTCCAAAG	AAAATATCAA	TCTATTAACT	GATGGTATGC	AACAAGTCGT	650
AAATAAAACA	CATAAAGAAG	ATATTTATAG	ATCTTATGCA	AACTTAATTG	700
GCAAATCCGG	TACTGCAGAA	CTCAAAATGA	AACAAGGAGA	AACTGGCAGA	750
CAAATTGGGT	GGTTTATATC	ATATGATAAA	GATAATCCAA	ACATGATGAT	800
GGCTATTAAT	GTTAAAGATG	TACAAGATAA	AGGAATGGCT	AGCTACAATG	850
CCAAAATCTC	AGGTAAAGTG	TATGATGAGC	TATATGAGAA	CGGTAATAAA	900
AAATACGATA	TAGATGAATA	ACAAAACAGT	GAAGCAATCC	GTAACGATGG	950
TTGCTTCACT	GTTTTATTAT	GAATTATTAA	TAAGTGCTGT	TACTTCTCCC	1000
TTAAATACAA	TTTCTTCATT	TTCATTGTAT	GTTGAAAGTG	ACACTGTAAC	1050
GAGTCCATTT	TCTTTTTTTA	TGGATTTCTT	ATTTGTAATT	TCAGCGATAA	1100
CGTACAATGT	ATTACCTGGG	TATACAGGTT	TAATAAATTT	AACGTTATTC	1150
ATTTGTGTTT	CTGCTACAAC	TTCTTCTCCG	TATTTACCTT	CTTCTACCCA	1200
TAATTTAAAT	GATATTGAAA	GTGTATGCAT	GCCAGATGCA	ATGATACCTT	1250
TAAATCTACT	TTGTTCTGCT	TTTTCTTTAT	CTATATGCAT	ATATTGAGGA	1300
TCAAAAGTTG	TTGCAAATTG	GATAAATTTCT	TCTTCTGTAA	TATGAAGGCT	1350
TTTTGTTTTG	AATGTTTCTC	CTACTATAAA	ATCATCGTAT	TTCATATATG	1400
TCTCTCTTTC	TTATTCAAAT	TAATTTTTTTA	GTATGTAACA	TGTTAAAGGT	1450
AAGTCTACCG	TCACTGAAAC	GTAAGACTCA	CCTCTAACTT	TCTATTGAGA	1500
CAAATGCACC	ATTTTATCTG	CATTGTCTGT	AAAGATACCA	TCAACTCCCC	1550
AATTAGCAAG	TTGGTTTGCA	CGTGCTGGTT	TGTTTACAGT	CCATACGTTT	1600
AATTCATAAC	CCGCTTCTTT	TACCATTTTTT	ACTTTTGCTT	TAGTAAGTTT	1650
GGCATCTTCA	GTGTTTACTA	TTTTAGCATT	ACAGTAATCT	AAAAGTGTTT	1700
TCCAGTCTTC	ACGAAACGAA	GTTGTATGGA	ATATAACTGC	TCTGTTATAT	1750
TGTGGCATGA	TTTCTTCTGC	AAGTTTAAAC	AGCACAACAT	TAAAGCTTGA	1800
AATGAGCACT	TCTTGATTCT	GATTTAAGTT	TGTTAATTGT	TCTTCCACTT	1850
GCTTAACCAT	ACTTTTAGAA	AGTGCTAGTC	CATTCGGTCC	AGTAATACCT	1900
TTTAATTCTA	CATTTAAATT	CATATTATAT	TCATTTGCTA	TTTTTACTAC	1950
ATCATCGAAA	GTTGGCAAAT	GTTTCATCTT	GAATTTTTC	CCAAACCAAG	2000
ATCCTGCAGA	AGCATCTTTA	ATTTTCATCAT	AATTCAAATC	AGTTATTTCC	2050
CCGGACATAT	TTGTAGTCCG	TTCTAAATAA	TCATCATGAA	TGATAATCAG	2100
TTGTTTCATCT	TTTGTAATTG	CAACATCTAA	CTCCAACCAG	TTTATACCTT	2150
CTACTTCTGA	AGCAGCTTTA	AATGATGCAA	TTGTATTTTC	CGGAGCTTTA	2200
CTAGGTAATC	CTCTATGTCC	ATATACAGTT	AGCATATTAC	CTCTCCTTGC	2250
ATTTTTATTT	TTTTAATTAA	CGTAACTGTA	TTATCACATT	AATCGCACTT	2300
TTATTTCCAT	TAAAAAGAGA	TGAATATCAT	AAATAAAGAA	GTCGATAGAT	2350
TCGTATTGAT	TATGGAGTTA	ATCTACGTCT	CATCTCATTT	TTAAAAAATC	2400
ATTTATGTCC	CAAGCTCCAT	TTTGTAATCA	AGTCTA		2436

2) INFORMATION FOR SEQ ID NO: 32

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 bases

(B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32

CGCTTGCCAC ATCAAATGAT GCGGGTTGTG CAAGCG

36

2) INFORMATION FOR SEQ ID NO: 33

(i) (A) LENGTH: 336 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Staphylococcus epidermidis
 (B) STRAIN: G3
 (C) ACCESSION NUMBER: SEQ ID NO:15, US PATENT 6,156,507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33

CTCATTACTT	ATGATAAGCT	TCTTAAAAAC	ATAACAGCAA	TTCACATAAA	50
CCTCATATGT	TCTGATACAT	TCAAAATCCC	TTTATGAAGC	GGCTGAAAAA	100
ACCGCATCAT	TTATGATATG	CTTCGCCTCT	CATGATCTTA	AATGCGCGAT	150
AAATTTGTTC	GATCAATATG	ACGCGCATAT	TTGGTGTGGG	AAGGTCATAT	200
TGCTAAAAGA	TAAAGCATAG	TTGCTGCGTT	GTAAGACGTC	TTGGTGTAAA	250
CCATTGGAGC	CACCTATGAC	AAATGTAAAG	TCGCTTTGAC	CTTGTGTCAT	300
GCGTGTTTGT	AGTTCTTTAG	CGAGTCCTTC	TGAAGA		336

2) INFORMATION FOR SEQ ID NO: 34

(i) (A) LENGTH: 260 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Staphylococcus haemolyticus
 (B) STRAIN: SH 518
 (C) ACCESSION NUMBER: SEQ ID NO:16, US PATENT 6,156,507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34

CTCATTACTT	ATGATAAGCT	TCTTAAAAAC	ATAACAGCAA	TCCACATAAA	50
CCTCATATGT	TCTGATACAT	TCAAAATCCC	TTTATGAAGC	GGCTGAAAAA	100
ACCGCATCAT	TTATGATATG	CTTCCCTCGC	ATGATTTTAA	ATGCTCTGTA	150
TACTTGCTCG	ATTAAGACAA	CGCGCATCAT	TTGATGTGGG	AATGTCATTT	200
TACTGAATGA	AAGTGCGTAG	TTGCTGCGTT	GTAAGACGTC	CTCATGCAAT	250
CCATTTGATC					260

2) INFORMATION FOR SEQ ID NO: 35

- (i) (A) LENGTH: 225 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: ATCC 25923
- (C) ACCESSION NUMBER: SEQ ID NO:9, US PATENT 6,156,507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35

TTCGTCATTG	GCGGATCAAA	CGGCCTGCAC	AAGGACGTCT	TACAACGCAG	50
TAACTACGCA	CTATCATTCA	GCAAAATGAC	ATTCCCACAT	CAAATGATGC	100
GGGTTGTGTT	AATTGAACAA	GTGTACAGAG	CATTTAAGAT	TATGCGTGGA	150
GAGGCGTATC	ACAAATAAAA	CTAAAAATGG	AGTAACTATT	AATATAGTAT	200
AAATTCAATA	TGGTGATAAA	AACAG			225

2) INFORMATION FOR SEQ ID NO: 36

- (i) (A) LENGTH: 225 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: STP23
- (C) ACCESSION NUMBER: SEQ ID NO:10 US PATENT 6,156,507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36

TTCGTCATTG	GCGGATCAAA	CGGCCTGCAC	AAGGACGTCT	TACAACGCAG	50
TAACTACGCA	CTATCATTCA	GCAAAATGAC	ATTCCCACAT	CAAATGATGC	100
GGGTTGTGTT	AATTGAACAA	GTGTACAGAG	CATTTAAGAT	TATGCGTGGA	150
GAGGCGTATC	ACAAATAAAA	CTAAAAATGG	AGTAACTATT	AATATAGTAT	200
AAATTCAATA	TGGTGATAAA	AACAG			225

2) INFORMATION FOR SEQ ID NO: 37

- (i) (A) LENGTH: 225 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: STP43
- (C) ACCESSION NUMBER: SEQ ID NO:12 US PATENT 6,156,507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37

TTCGTCATTG	GCGGATCAAA	CGGCCTGCAC	AAGGACGTCT	TACAACGTAG	50
TAACTACGCA	CTATCATTCA	GCAAAATGAC	ATTTCACAT	CAAATGATGC	100
GGGTTGTGTT	AATTGAACAA	GTGTACAGAG	CATTTAAGAT	TATGCGTGGA	150
GAGGCGTATC	ATAAGTAATG	AGGTTTCATGA	TTTTTGACAT	AGTTAGCCTC	200
CGCAGTCTTT	CAAGTAAATA	ATATC			225

2) INFORMATION FOR SEQ ID NO: 38

- (i) (A) LENGTH: 225 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: STP53
- (C) ACCESSION NUMBER: SEQ ID NO:13 US PATENT 6,156,507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38

TTCGTCATTG	GCGGATCAAA	CGGCCTGCAC	AAGGACGTCT	TACAACGCAG	50
TAACTACGCA	CTATCATTTA	GCAAAATGAC	ATTCCCACAT	CAAATGATGC	100
GGGTTGTGTT	AATTGAACAA	GTGTATAGAG	CATTTAAGAT	TATGCGTGGA	150
GAGGCGTATC	ATAAGTGATG	CTTGTTAGAA	TGATTTTAA	CAATATGAAA	200

TAGCTGTGGA AGCTCAAACA TTTGT

225

2) INFORMATION FOR SEQ ID NO: 39

- (i) (A) LENGTH: 1500 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: 476
- (C) ACCESSION NUMBER: Extracted from Genome project

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39

TGAGTCTGGT	AAAGATACAC	AACCAATTGG	TAAAGAGAAA	GTGATGAATC	50
CAGCGAAACA	ACCAGCGACA	GGTAAAGTTG	TGTTGTTACC	AGCGCATAGA	100
GGAAGTGTTA	GTAGCGGTAC	AGAAGGTTCT	GATCGCGCAT	TAGAAGGAAC	150
TGCTGTATCA	AGTAAGAGTG	GGAAACAATT	GGCTAACATG	TCAGCGCCTA	200
AAGGTAGCGC	ACATGAGAAA	CAGTTACCAA	AAACTGGAAC	TGATCAAAGT	250
TCAAGCCCAG	CAGCGATGTT	TGTATTAGTA	ACAGGTATAG	GTTTAATCGC	300
GACTGTACGA	CGTAGAAAAG	CTAGCTAAAA	TATATTGAAA	ACAATACTAC	350
TGTATTTCTT	AAATAAGAGG	TACGGTAGTG	TTTTTTTATG	GAAAAAAGCT	400
ATAACCGTTG	ATAAATATGG	GATATAAAAA	CGGGGATAAG	TAATAAGACA	450
TCAAGGTATT	TATCCACAGA	AATGGGGATA	GTTATCCAGA	ATTGTGTACA	500
ATTTAAAGAG	AAATACCCAC	AATGCCCCAC	GAGTTATCCA	CAAATACACA	550
AGTTATACAC	TGAAAATTGG	GCATGAATGT	CAGAAAAATA	TCAAAAACCTG	600
CAAAAAAACT	TGGTATAATA	AGAGGGGAAA	GTGTGAACAA	GTTAATAACT	650
TGTGGATAAC	TGGAAAGTTG	ATAACAATTT	GGAGGACCAA	ACGACATGAA	700
AATCACCATT	TTAGcTGTAG	GGAAACTAAA	AGAGAAATAT	TGGAAGCAAG	750
CCATAGCAGA	ATATGAAAAA	CGTTTAGGCC	CATACACCAA	GATAGACATC	800
ATAGAAGTTA	CAGACGAAAA	AGCACCAGAA	AATATGAGCG	ACAAAGAAAT	850
CGAGCAAGTA	AAAGAAAAAG	AAGGCCAACG	AATACTAGCC	AAAATCAAAC	900
CACAATCCAC	AGTCATTACA	TTAGAAATAC	AAGGAAAAGAT	GCTATCTTCC	950
GAAGGATTGG	CCCAAGAATT	GAACCAACGC	ATGACCCAAG	GGCAAAGCGA	1000
CTTTGTATTG	GTCATTGGCG	GATCAAACGG	CCTGCACAAG	GACGTCTTAC	1050
AACGTAGTAA	CTACGCACTA	TCATTCAGCA	AAATGACATT	TCCACATCAA	1100
ATGATGCGGG	TTGTGTTAAT	TGAACAAGTG	TACAGAGCAT	TTAAGATTAT	1150
GCGTGGAGAA	GCTTATCATA	AATGATGCGG	TTTTTTCTTG	AAAAATTTAA	1200
TTAGATATTA	GAATCCTTTA	ATTTATTTGA	AAATCAGAAG	TGAGTAACAA	1250
TGGTAAGTGA	AATAGTTAGT	GCAATAATTG	GAATTATAGG	GATTTATTGA	1300
GATGTATGGA	GATGCGGGGC	ATTTATCGAG	TAGATTACAA	TTAGAGCATG	1350
TAGGTGATTT	GCTTTTTTCAT	GCAAGTAAAG	ATAAACTTTT	AAAAATCCTA	1400
TAAGAATTTA	GAAACTTTAG	AATAACTAAA	TATTAAAAAA	ATATCGTATG	1450
AAAGTGAAAT	TAGGATGAGA	GACCATAGCT	AAATTAAAAA	TTTTAGCAAA	1500

2) INFORMATION FOR SEQ ID NO: 40

- (i) (A) LENGTH: 1501 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: 252
- (C) ACCESSION NUMBER: Extracted from Genome project

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40

TTGCACAACC	AATTGGTAAA	GACAAAGTGA	TGGATCCAGC	GAAACAACCA	50
GCGCCAAGTA	AAGTTGTATT	GTTGCCAGCG	CATAGAGGAA	CTGTTAGTAG	100
TGGTAGAGAA	GGTTCGTGATC	GCGCATTTGA	AGGAACTGCT	GTATCAAGTA	150
AGAGCGGGAA	ACAATTGGCT	AGCATGTCAG	CGCCTAAAGG	TAGCACACAT	200
GAGAAGCAGT	TACCAAAAAC	TGGAAGTGAT	CAAAGTTCAA	GCCCAGCAGC	250
GATGTTTGT	TTAGTAGCAG	GTATAGGTTT	AATTGCGACT	GTACGACGTA	300
GAAAAGCTAG	CTAAAATATA	TTGAAAACAA	TACTACTGTA	TTTCTTAAAC	350
AAGAGGTACG	GTAGTGTTTT	TTTATGAAAA	AAAGCTATAA	CCGTTGATAA	400
ATATGGGATA	TAAAAACGGG	GATAAGTAAT	AAGACATCAA	GGTATTTATC	450
CACAGAAATG	GGGATAGTTA	TCCAGAATTG	TGTACAATTT	AAAGAGAAAT	500
ACCCACAATG	CCCACAGAGT	TATCCACAAA	TACACAGGTT	ATACACTAAA	550
AATTGGGCAT	GAATGTCAGA	AAAATATCAA	AAACTGCAAA	GAATATTGGT	600
ATAATAAGAG	GGAACAGTGT	GAACAAGTTA	ATAACTTGTTG	GATAACTGGA	650
AAGTTGATAA	CAATTTGGAG	GACCAAACGA	CATGAAAATC	ACCATTTTAG	700
CTGTAGGGAA	ACTAAAAGAG	AAATATTGGA	AGCAAGCCAT	AGCAGAATAT	750
GAAAAACGTT	TAGGCCCAT	CACCAAGATA	GACATCATAG	AAGTTCCAGA	800
CGAAAAAGCA	CCAGAAAATA	TGAGCGACAA	AGAAATTGAG	CAAGTAAAAG	850
AAAAAGAAGG	CCAACGAATA	CTAGCCAAAA	TCAAACCACA	ATCAACAGTC	900
ATTACATTAG	AAATACAAGG	AAAGATGCTA	TCTTCCGAAG	GATTGGCCCA	950
AGAATTGAAC	CAACGCATGA	CCCAAGGGCA	AAGCGACTTT	GTATTTCGTCA	1000
TTGGCGGATC	AAACGGCCTG	CACAAGGACG	TCTTACAACG	CAGTAACTAC	1050
GCACTATCAT	TCAGCAAAAT	GACATTCCCA	CATCAAATGA	TGCGGGTTGT	1100
GTTAATTGAA	CAAGTGTACA	GAGCATTTAA	GATTATGCGT	GGAGAAGCAT	1150
ATCATAAATG	ATGCGGTTTT	TTCAGCCGCT	TCATAAAGGG	ATTTTGAATG	1200
TATCAGAACA	TATGAGGTTT	ATGTGAATTG	CTGTTATGTT	TTTAAGAAGC	1250
TTATCATAAG	TAATGAGGTT	CATGATTTTT	GACATAGTTA	GCCTCCGCAG	1300
TCTTTCATTT	CAAGTAAATA	ATAGCGAAAT	ATTCTTTATA	CTGAATACTT	1350
ATAGTGAAGC	AAAGTTCTAG	CTTTGAGAAA	ATTCTTTCTG	CAACTAAATA	1400
TAGTAAATTA	CGGTAAATA	TAAATAAGTA	CATATTGAAG	AAAATGAGAC	1450
ATAATATATT	TTATAATAGG	AGGGAATTTT	AAATGATAGA	CAACTTTATG	1500
C					1501

2) INFORMATION FOR SEQ ID NO: 41

- (i) (A) LENGTH: 2480 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: COL
- (C) ACCESSION NUMBER: Extracted from Genome project

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41

AAACCGTCTG	GCAAACGAAT	TAATGCTATT	CAAATTTTAA	ATAAAGAGAC	50
AGGTAAGTTT	GAAAATATTG	ATTTAAAACG	TGTATATCAC	GTAACGATGA	100
ATGACTTCAC	AGCATCAGGT	GGCGACGGAT	ATAGTATGTT	CGGTGGTCCT	150
AGAGAAGAAG	GTATTTTCATT	AGATCAAGTA	CTAGCAAGTT	ATTTAAAAAC	200
AGCTAACTTA	GCTAAGTATG	ATACGACAGA	ACCACAACGT	ATGTTATTAG	250
GTAACCAGC	AGTAAGTGAA	CAACCAGCTA	AAGGACAACA	AGGTAGCAAA	300
GGTAGTAAGT	CTGGTAAAGA	TACACAACCA	ATTGGTGACG	ACAAAGTGAT	350
GGATCCAGCG	AAAAAACCCAG	CTCCAGGTAA	AGTTGTATTG	TTGCTAGCGC	400
ATAGAGGAAC	TGTTAGTAGC	GGTACAGAAG	GTTCTGGTCG	CACAATAGAA	450
GGAGCTACTG	TATCAAGCAA	GAGTGGGAAA	CAATTGGCTA	GAATGTCAGT	500
GCCTAAAGGT	AGCGCGCATG	AGAAACAGTT	ACCAAAAAC	GGAACATAATC	550
AAAGTTCAAG	CCCAGAAGCG	ATGTTTGTAT	TATTAGCAGG	TATAGGTTTA	600
ATCGCGACTG	TACGACGTAG	AAAAGCTAGC	TAAAATATAT	TGAAAATAAT	650
ACTACTGTAT	TTCTTAAATA	AGAGGTACGG	TAGTGTTTTT	TTATGAAAAA	700
AAGCGATAAC	CGTTGATAAA	TATGGGATAT	AAAAACGAGG	ATAAGTAATA	750
AGACATCAAG	GTGTTTATCC	ACAGAAATGG	GGATAGTTAT	CCAGAATTGT	800
GTACAATTTA	AAGAGAAATA	CCCACAATGC	CCACAGAGTT	ACCCACAAAT	850
ACACAGGTTA	TACACTAAAA	ATCGGGCATA	AATGTCAGGA	AAATATCAAA	900
AACTGCAAAA	AATATTGGTA	TAATAAGAGG	GAACAGTGTG	AACAAGTTAA	950
TAACTTGTGG	ATAACTGGAA	AGTTGATAAC	AATTTGGAGG	ACCAAACGAC	1000
ATGAAAATCA	CCATTTTAGC	TGTAGGGAAA	CTAAAAGAGA	AATATTGGAA	1050
GCAAGCCATA	GCAGAATATG	AAAAACGTTT	AGGCCCATAC	ACCAAGATAG	1100
ACATCATAGA	AGTTCCAGAC	GAAAAAGCAC	CAGAAAATAT	GAGTGACAAA	1150
GAAATTGAGC	AAGTAAAAGA	AAAAGAAGGC	CAACGAATAC	TAGCCAAAAT	1200
CAAACCACAA	TCCACAGTCA	TTACATTAGA	AATACAAGGA	AAGATGCTAT	1250
CTTCCGAAGG	ATTGGCCCAA	GAATTGAACC	AACGCATGAC	CCAAGGGCAA	1300
AGCGACTTTG	TTTTCGTCAT	TGGCGGATCA	AACGGCCTGC	ACAAGGACGT	1350
CTTACAACGC	AGTAACTACG	CACTATCAT	CAGCAAAATG	ACATTCCCAC	1400
ATCAAATGAT	GCGGGTTGTG	TTAATTGAAC	AAGTGTACAG	AGCATTTAAG	1450
ATTATGCGAG	GAGAAGCTTA	TCATAAGTAA	TGAGGTTTAT	GATTTTTTGAC	1500
ATAGTTAGCC	TCCGCAGTCT	TTCATTTCAA	GTAAATAATA	GCGAAATATT	1550
CTTTTACTG	AATACTTATA	GTGAAGCAAA	GTTCTAGCTT	TGAGAAAATT	1600
CTTTCTGCAA	CTAAATATAG	TAAATTACGG	TAAAATATAA	ATAAGTACAT	1650
ATTGAAGAAA	ATGAGACATA	ATATATTTTA	TAATAGGAGG	GAATTTCAAA	1700
TGATAGACAA	CTTTATGCAG	GTCCTTAAAT	TAATTAAAGA	GAAACGTACC	1750
AATAATGTAG	TTAAAAAATC	TGATTGGGAT	AAAGGTGATC	TATATAAAAC	1800
TTTAGTCCAT	GATAAGTTAC	CCAAGCAGTT	AAAAGTGCAT	ATAAAAGAAG	1850

ATAAATATTC	AGTTGTAGGG	AAGGTTGCTA	CTGGGAACTA	TAGTAAAGTT	1900
CCTTGGATTT	CAATATATGA	TGAGAATATA	ACAAAAGAAA	CAAAGGATGG	1950
ATATTATTTG	GTATATCTTT	TTCATCCGGA	AGGAGAAGGC	ATATACTTAT	2000
CTTTGAATCA	AGGATGGTCA	AAGATAAGTG	ATATGTTTCC	GCGGGATAAA	2050
AATGCTGCAA	AACAAAGAGC	ATTAAC TT TA	TCTTCCGAAC	TCAATAAATA	2100
TATTACATCA	AATGAATT TA	ATACTGGAAG	ATTTTATTAC	GCAGAAAATA	2150
AAGATTCATC	TTATGATT TA	AAAAATGATT	ATCCATCAGG	ATATTCTCAT	2200
GGATCAATAA	GATTCAAATA	TTATGATTTG	AATGAAGGAT	TCACAGAAGA	2250
AGATATGCTA	GAGGATTTAA	AGAAATTTTT	AGA ACT ATTT	AATGAATTAG	2300
CTTCAAAAGT	TACAAAAACA	TCCTATGATA	GCTTGGTCAA	TAGCATAGAC	2350
GAAATACAGG	AAGACAGCGA	AATTGAAGAA	ATTAGAACAG	CACAAAAAGA	2400
TAAGACACTC	AAGGAAGTGG	AAGCACCTAA	AGGAATAATT	CCAAAATATA	2450
AAAAAGGTGT	ATCAAAGACT	ACTAAAAATG			2480

2) INFORMATION FOR SEQ ID NO: 42

- (i) (A) LENGTH: 1045 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: ATCC 33592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42

CCAGTTTTTTT	GTTTAATGAA	CAAGGTAAAT	TACGAGATAA	TATTTGAAGA	50
AAACAATAAA	GTAGAGATGG	ATTTCCATAT	CCTCTTTAGT	AGCGGTTTTT	100
ATCTGTAAGG	TTTATTAATA	ATTAAATAAA	TAGGCGGGAT	AGTTATATAT	150
AGCTTATTAA	TGAAAGAATA	TGATTATTAA	TTTAGTATTA	TATTTTAATA	200
TTAAAAAGAA	GATATGAAAT	AATTATTTCAT	ACCTTCCACC	TTACAATAAT	250
TAGTTTTTCAA	TCGAATATTA	AGATTATTAG	TAGTCTTAAA	AGTTAAGACT	300
TCCTTATATT	AATGACCTAA	TTTATTATTT	GCCTCATGAA	TTATCTTTTT	350
ATTTCTTTGA	TATGTCCCAA	ACCACATCGT	GATATACACT	ACAATAAATA	400
TTATGATGAA	ACTAATAATA	TTCTCAAAGT	TCAGATGGAA	CCAACCTGCT	450
AGAATAGCGA	GTGGGAAGAA	TAGGATTATC	ATCAATATAA	AGTGA ACTAC	500
AGTCTGTTTT	GTTATACTCC	AATCGGTATC	TGTAAATATC	AAATTACCAT	550
AAGTAAACAA	AATTCCAATC	AATGCCCATA	GTGCTACACA	TATTAGCATA	600
ATAACCGCTT	CATTAAAGTT	TTCATAATAA	ATTTTACCCA	TAAAAGAATC	650
TGGATATAGT	GGTACATATT	TATCCCTTGA	AAAAAATAAG	TGAAGTAATG	700
ACAGAAATCA	TAAGACCAGT	GAACGCACCT	TTTTGAACAG	CGTGGAATAA	750
TTTTTTTCATA	GTGAGATGGA	CCATTCCATT	TGTTTCTAAC	TTCAAGTGAT	800
CAATGTAATT	TAGATTGATA	ATTTCTGATT	TTGAAATACG	CACGAATATT	850
GAACCGACAA	GCTCTTCAAT	TTGGTAAAGT	CGCTGATAAA	GTTTTAAAGC	900
TTTATTATTC	ATTGTTATCG	CATACCTGTT	TATCTTCTAC	TATGAAC TGT	950
GCAATTTGTT	CTAGATCAAT	TGGGTAAACA	TGATGGTTCT	GTTGCAAAGT	1000
AAAAAAATAT	AGCTAACCAC	TAATTTATCA	TGTCAGTGTT	CGCTT	1045

2) INFORMATION FOR SEQ ID NO: 43

- (i) (A) LENGTH: 1118 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Staphylococcus aureus
 (B) STRAIN: CCRI-8895
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43

CAGAGCATT	T	AAGATTATGC	GTGGAGAAGC	GTACCACAAA	TGATGCGGTT	50
TTTTATCCAG	T	TTTTTTGTTT	AATGAACAAG	GTAAATTACG	AGATAATATT	100
TGAAGAAAAC	A	AATAAAGTAG	AGATGGATT	CCATATCCTC	TTTAGTAGCG	150
GTTTTTATCT	G	TAAAGGTTTA	TTAATAATTA	AATAAATAGG	CGGGATAGTT	200
ATATATAGCT	T	TATTAATGAA	AGAATATGAT	TATTAATTTA	GTATTATATT	250
TTAATATTAA	AA	AGAAGATA	TGAAATAATT	ATTCATACCT	TCCACCTTAC	300
AATAATTAGT	T	TTCAATCGA	ATATTAAGAT	TATTAGTAGT	CTTAAAAGTT	350
AAGACTTCCT	T	ATATTAATG	ACCTAATTTA	TTATTTGCCT	CATGAATTAT	400
CTTTTTATTT	C	TTTGATATG	TCCCAAACCA	CATCGTGATA	TACACTACAA	450
TAAATATTAT	G	ATGAAACTA	ATAATATTCT	CAAAGTTCAG	ATGGAACCAA	500
CCTGCTAGAA	T	AGCGAGTGG	GAAGAATAGG	ATTATCATCA	ATATAAAGTG	550
AACTACAGTC	T	GTTTTTGTTA	TACTCCAATC	GGTATCTGTA	AATATCAAAT	600
TACCATAAGT	AA	ACAAAAT	CCAATCAATG	CCCATAGTGC	TACACATATT	650
AGCATAATAA	C	CGCTTCATT	AAAGTTTTCA	TAATAAATTT	TACCCATAAA	700
AGAATCTGGA	T	ATAGTAGTA	CATATTTATC	CCTTGAAAAA	AATAAGTGAA	750
GTAATGACAG	AA	ATCATAAG	ACCAGTGAAC	GCACCTTTTT	GAACAGCGTG	800
GAATAATTTT	T	TCATAGTGA	GATGGACCAT	TCCATTTGTT	TCTAACTTCA	850
AGTGATCAAT	G	TAATTTAGA	TTGATAATTT	CTGATTTTGA	AATACGCACG	900
AATATTGAAC	C	GACAAGCTC	TTCAATTTGG	TAAAGTCGCT	GATAAAGTTT	950
TAAAGCTTTA	T	TATTCATTG	TTATCGCATA	CCTGTTTATC	TTCTACTATG	1000
AACTGTGCAA	T	TGTTCCTAG	ATCAATTGGG	TAAACATGAT	GGTTCTGTTG	1050
CAAAGTAAAA	AA	ATATAGCT	AACCACTAAT	TTATCATGTC	AGTGTTGCTG	1100
TAACCTTGCTA	G	CATGATG				1118

2) INFORMATION FOR SEQ ID NO: 44

- (i) (A) LENGTH: 1118 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Staphylococcus aureus
 (B) STRAIN: CCRI-8903
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44

CAGAGCATTT	AAGATTATGC	GTGGAGAAGC	GTACCACAAA	TGATGCGGTT	50
TTTTATCCAG	TTTTTTTGTTT	AATGAACAAG	GTAAATTACG	AGATAATATT	100
TGAAGAAAAC	AATAAAGTAG	AGATGGATT	CCATATCCTC	TTTAGTAGCG	150
GTTTTTATCT	GTAAGGTTTA	TTAATAATTA	AATAAATAGG	CGGGATAGTT	200
ATATATAGCT	TATTAATGAA	AGAATATGAT	TATTAATTTA	GTATTATATT	250
TTAATATTAA	AAAGAAGATA	TGAAATAATT	ATTCATACCT	TCCACCTTAC	300
AATAATTAGT	TTTCAATCGA	ATATTAAGAT	TATTAGTAGT	CTTAAAAGTT	350
AAGACTTCCT	TATATTAATG	ACCTAATTTA	TTATTTGCCT	CATGAATTAT	400
CTTTTTATTT	CTTTGATATG	TCCCAAACCA	CATCGTGATA	TACACTACAA	450
TAAATATTAT	GATGAAACTA	ATAATATTCT	CAAAGTTCAG	ATGGAACCAA	500
CCTGCTAGAA	TAGCGAGTGG	GAAGAATAGG	ATTATCATCA	ATATAAAGTG	550
AACTACAGTC	TGTTTTGTTA	TACTCCAATC	GGTATCTGTA	AATATCAAAT	600
TACCATAAGT	AAACAAAATT	CCAATCAATG	CCCATAGTGC	TACACATATT	650
AGCATAATAA	CCGCTTCATT	AAAGTTTTCA	TAATAAATTT	TACCCATAAA	700
AGAATCTGGA	TATAGTAGTA	CATATTTATC	CCTTGAAAAA	AATAAGTGAA	750
GTAATGACAG	AAATCATAAG	ACCAGTGAAC	GCACCTTTTT	GAACAGCGTG	800
GAATAATTTT	TTCATAGTGA	GATGGACCAT	TCCATTTGTT	TCTAACTTCA	850
AGTGATCAAT	GTAATTTAGA	TTGATAATTT	CTGATTTTGA	AATACGCACG	900
AATATTGAAC	CGACAAGCTC	TTCAATTTGG	TAAAGTCGCT	GATAAAGTTT	950
TAAAGCTTTA	TTATTCATTG	TTATCGCATA	CCTGTTTATC	TTCTACTATG	1000
AACTGTGCAA	TTTGTTCTAG	ATCAATTGGG	TAAACATGAT	GGTTCTGTTG	1050
CAAAGTAAAA	AAATATAGCT	AACCACTAAT	TTATCATGTC	AGTGTTTCGCT	1100
TAACTTGCTA	GCATGATG				1118

2) INFORMATION FOR SEQ ID NO: 45

- (i) (A) LENGTH: 1113 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-1324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45

AGCATTTAAG	ATTATGCGTG	GAGAAGCGTA	CCACAAATGA	TGCGGTTTTT	50
TATCCAGTTT	TTTGTTTAAT	GAACAAGGTA	AATTACGAGA	TAATATTTGA	100
AGAAAACAAT	AAAGTAGAGA	TGGATTTCCA	TATCCTCTTT	AGTAGCGGTT	150
TTTATCTGTA	AGGTTTATTA	ATAATTAAAT	AAATAGGCGG	GATAGTTATA	200
TATAGCTTAT	TAATGAAAGA	ATATGATTAT	TAATTTAGTA	TTATATTTTA	250
ATATTAAAAA	GAAGATATGA	AATAATTAT	CATACCTTCC	ACCTTACAAT	300
AATTAGTTTT	CAATCGAATA	TTAAGATTAT	TAGTAGTCTT	AAAAGTTAAG	350
ACTTCCTTAT	ATTAATGACC	TAATTTATTA	TTTGCCTCAT	GAATTATCTT	400
TTTATTTCTT	TGATATGTCC	CAAACCACAT	CGTGATATAC	ACTACAATAA	450
ATATTATGAT	GAAACTAATA	ATATTCTCAA	AGTTCAGATG	GAACCAACCT	500
GCTAGAATAG	CGAGTGGGAA	GAATAGGATT	ATCATCAATA	TAAAGTGAAC	550
TACAGTCTGT	TTTGTTTATAC	TCCAATCGGT	ATCTGTAAAT	ATCAAATTAC	600
CATAAGTAAA	CAAAATTCCA	ATCAATGCCC	ATAGTGCTAC	ACATATTAGC	650
ATAATAACCG	CTTCATTAAA	GTTTTTCATA	TAAATTTTAC	CCATAAAAGA	700
ATCTGGATAT	AGTGGTACAT	ATTTATCCCT	TGAAAAAAT	AAGTGAAGTA	750

ATGACAGAAA	TCATAAGACC	AGTGAACGCA	CCTTTTTTGAA	CAGCGTGGAA	800
TAATTTTTTC	ATAGTGAGAT	GGACCATTC	ATTTGTTTCT	AACTTCAAGT	850
GATCAATGTA	ATTTAGATTG	ATAATTTCTG	ATTTTGAAAT	ACGCACGAAT	900
ATTGAACCGA	CAAGCTCTTC	AATTTGGTAA	AGTCGCTGAT	AAAGTTTTAA	950
AGCTTTATTA	TTCATTGTTA	TCGCATACCT	GTTTATCTTC	TACTATGAAC	1000
TGTGCAATTT	GTTCTAGATC	AATTGGGTAA	ACATGATGGT	TCTGTTGCAA	1050
AGTAAAAAAA	TATAGCTAAC	CACTAATTTA	TCATGTCAGT	GTTTCGCTTAA	1100
CTTGCTAGCA	TGA				1113

2) INFORMATION FOR SEQ ID NO: 46

- (i) (A) LENGTH: 2153 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: CCRI-1331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46

CTGTAGGGAA	ACTAAAAGAG	AAATACTGGA	AGCAAGCCAT	AGCAGAATAT	50
GAAAAACGTT	TAGGCCCAT	CACCAAGATA	GACATCATAG	AAGTTCCAGA	100
CGAAAAAGCA	CCAGAAAATA	TGAGCGACAA	AGAAATCGAG	CAAGTAAAAG	150
AAAAAGAAGG	CCAACGAATA	CTAGCCAAAA	TCAAACCACA	ATCCACAGTC	200
ATTACATTAG	AAATACAAGG	AAAGATGCTA	TCTTCCGAAG	GATTGGCCCA	250
AGAATTGAAC	CAACGCATGA	CCCAAGGGCA	AAGCGACTTT	GTATTCGTCA	300
TTGGCGGATC	AAACGGCCTG	CACAAGGACG	TCTTACAACG	CAGTAACTAC	350
GCACTATCAT	TCAGCAAAAT	GACATTCCCA	CATCAAATGA	TGCGGGTTGT	400
GTTAATTGAA	CAAGTGTACA	GAGCATTTAA	GATTATGCGT	GGAGAAGCGT	450
ACCACAAATG	ATGCGGTTTT	TTATCCAGTT	TTTTGTTTAA	TGAACAAGGT	500
AAATTACGAG	ATAATATTTG	AAGAAAACAA	TAAAGTAGAG	ATGGATTTCC	550
ATATCCTCTT	TAGTAGCGGT	TTTTATCTGT	AAGGTTTATT	AATAATTAAA	600
TAAATAGGCG	GGATAGTTAT	ATATAGCTTA	TTAATGAAAG	AATATGATTA	650
TTAATTTAGT	ATTATATTTT	AATATTAAAA	AGAAGATATG	AAATAATTAT	700
TCATACCTTC	CACCTTACAA	TAATTAGTTT	TCAATCGAAT	ATTAAGATTA	750
TTAGTAGTCT	TAAAAGTTAA	GACTTCCTTA	TATTAATGAC	CTAATTTATT	800
ATTTGCCTCA	TGAATTATCT	TTTTATTTCT	TTGATATGTC	CCAAACCACA	850
TCGTGATATA	CACTACAATA	AATATTATGA	TGAAACTAAT	AATATTCTCA	900
AAGTTCAGAT	GGAACCAACC	TGCTAGAATA	GCGAGTGGGA	AGAATAGGAT	950
TATCATCAAT	ATAAAGTGAA	CTACAGTCTG	TTTTGTTTATA	CTCCAATCGG	1000
TATCTGTAAA	TATCAAATTA	CCATAAGTAA	ACAAAATTCC	AATCAATGCC	1050
CATAGTGCTA	CACATATTAG	CATAATAACC	GCTTCATTAA	AGTTTTTCATA	1100
ATAAATTTTA	CCCATAAAAG	AATCTGGATA	TAGTGGTACA	TATTTATCCC	1150
TTGAAAAAAA	TAAGTGAAGT	AATGACAGAA	ATCATAAGAC	CAGTGAACGC	1200
ACCTTTTTGA	ACAGCGTGGA	ATAATTTTTT	CATAGTGAGA	TGGACCATTC	1250
CATTTGTTTC	TAACTTCAAG	TGATCAATGT	AATTTAGATT	GATAATTTCT	1300
GATTTTGAAA	TACGCACGAA	TATTGAACCG	ACAAGCTCTT	CAATTTGGTA	1350
AAGTCGCTGA	TAAAGTTTTA	AAGCTTTATT	ATTCATTGTT	ATCGCATACC	1400
TGTTTATCTT	CTACTATGAA	CTGTGCAATT	TGTTCTAGAT	CAATTGGGTA	1450
AACATGATGG	TTCTGTTGCA	AAGTAAAAAA	ATATAGCTAA	CCACTAATTT	1500
ATCATGTCAG	TGTTTCGCTTA	ACTTGCTAGC	ATGATGCTAA	TTTCGTGGCA	1550

TGGCGAAAAAT	CCGTAGATCT	GATGAGACCT	GCGGTTCTTT	TTATATAGAG	1600
CGTAAATACA	TTCAATACCT	TTTAAAGTAT	TCTTTGCTGT	ATTGATACTT	1650
TGATACCTTG	TCTTTCTTAC	TTTAATATGA	CGGTGATCTT	GCTCAATGAG	1700
GTTATTCAAA	TATTTTCGATG	TACAATGACA	GTCAGGTTTA	AGTTTAAAAG	1750
CTTTAATTAC	TTTAGCCATT	GCTACCTTCG	TTGAAGGTGC	CTGATCTGTA	1800
ATTACCTTTT	GAGGTTTACC	AAATTGTTTA	ATGAGACGTT	TAATAAACGC	1850
ATATGCTGAA	TGATTATCTC	GTTGCTTACG	CAACCAAATA	TCTAATGTAT	1900
GTCCCTCTGC	ATCAATGGCA	CGATATAAAT	AGCTCCATTT	TCCTTTTATT	1950
TTGATGTACG	TCTCATCAAT	ACGCCATTTG	TAATAAGCTT	TTTTATGCTT	2000
TTTCTTCCAA	ATTTGATATA	AAATTGGGGC	ATATTCTTGA	ACCCAACGGT	2050
AGACCGTTGA	ATGATGAACG	TTTACACCAC	GTCCCTTAA	TATTTTCAGAT	2100
ATATCACGAT	AACTCAATGC	ATATCTTAGA	TAGTAGCCAA	CGGCTACAGT	2150
GAT					2153

2) INFORMATION FOR SEQ ID NO: 47

- (i) (A) LENGTH: 737 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-1263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47

TTTAAGATTA	TGCGTGGAGA	AGCATATCAT	AAATGATGCG	GTTATTTTCAG	50
CCGTAATTTT	ATAATATAAA	GCAGAGTTTA	TTAAATTTTA	ATGATTACTT	100
TTTATTAAGA	ATTAATTCTA	GTTGATATAT	TATAATGTGA	AACACAAAAT	150
AATAATTTGT	AATTGTTAGT	TTATAGGCAT	CTGTATTTGG	AATTTTTTGT	200
AGACTATTTA	AAAAATAGTG	TATATAAGTA	TTGAGTTCAT	GTATTAAC TG	250
TCTTTTTTCA	TCGTTTCATCA	AGTATAAGGA	TGTAGAGATT	TGTTGGATAA	300
TTTCTTCGGA	TGTTTTTTAAA	ATTATCATTA	AATTAGATGG	TATCTGATCT	350
1 TGAGTTTGT	TTTTAGTGTA	TGTATATTTT	AAAAAATTTT	TGATTGTTGT	400
TATTTGACTC	TCTTTTAATT	TGACACCCTC	ATCAATAAAT	GTGTTAAATA	450
TATCTTCATT	TGTACTTAAA	TCATCAAAAAT	TTGCCAACAA	ATATTTGAAC	500
GTCTCTAAAT	CATTATGTTT	GAGTTCCGTT	TTGCTATTCC	ATAATTCCAA	550
ACCATTTGGT	AGAAAGCCCA	AGCTGTGATT	TTGATCTCCC	CATATAGCTG	600
AATTTAAATC	AGTGAGTTGA	TTAATTTTTT	CAACACAGAA	ATGTAATTTT	650
GGAATGAGGA	ATCGAAGTTG	TTCTTCTACT	TGCTGTACTT	TTCTTTTGT	700
TTCAATAAAA	TTTCTACACC	ATACTGTTAT	CAAACCG		737

2) INFORMATION FOR SEQ ID NO: 48

- (i) (A) LENGTH: 1592 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: CCRI-1377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48

AACTAAAAGA	GAAATATTGG	AAGCAAGCCA	TAGCAGAATA	TGAAAAACGT	50
TTAGGCCCAT	ACACCAAGAT	AGACATCATA	GAAGTTCCAG	ACGAAAAAGC	100
ACCAGAAAAT	ATGAGTGACA	AAGAAATTGA	GCAAGTAAAA	GAAAAAGAAG	150
GCCAACGAAT	ACTAGCCAAA	ATCAAACCAC	AATCCACAGT	CATTACATTA	200
GAAATACAAG	GAAAGATGCT	ATCTTCCGAA	GGATTGGCCC	AAGAATTGAA	250
CCAACGCATG	ACCCAAGGGC	AAAGCGACTT	TGTTTTTCGTC	ATTGGCGGAT	300
CAAACGGCCT	GCACAAGGAC	GTCTTACAAC	GCAGTAACTA	CGCACTATCA	350
TTCAGCAAAA	TGACATTCCC	ACATCAAATG	ATGCGGGTTG	TGTTAATTGA	400
ACAAGTGTA	AGAGCATTTA	AGATTATGCG	AGGAGAAGCA	TATCATAAAT	450
GATGCGGTTA	TTTCAGCCGT	AATTTTATAA	TATAAAGCAG	AGTTTATTAA	500
ATTTTAATGA	TTACTTTTTA	TTAAGAATTA	ATTCTAGTTG	ATATATTATA	550
ATGTGAAACA	CAAAATAATA	ATTTGTAAAT	GTTAGTTTAT	AGGCATCTGT	600
ATTTGGAATT	TTTTGTAGAC	TATTTAAAAA	ATAGTGTATA	TAAGTATTGA	650
GTTCATGTAT	TAAGTGTCTT	TTTTCATCGT	TCATCAAGTA	TAAGGATGTA	700
GAGATTTGTT	GGATAATTTC	TTCGGATGTT	TTTAAAAATTA	TCATTAAAT	750
AGATGGTATC	TGATCTTGAG	TTTTGTTTTT	AGTGTATGTA	TATTTTAAAA	800
AATTTTTGAT	TGTTGTTATT	TGACTCTCTT	TTAATTTGAC	ACCTCATCA	850
ATAAATGTGT	TAAATATATC	TTCATTTGTA	CTTAAATCAT	CAAAATTTGC	900
CAACAAATAT	TTGAACGTCT	CTAAATCATT	ATGTTTGAGT	TCCGTTTTGC	950
TATTCATAA	TTCCAAACCA	TTTGGTAGAA	AGCCCAAGCT	GTGATTTTGA	1000
TCTCCCCATA	TAGCTGAATT	TAAATCAGTG	AGTTGATTAA	TTTTTTCAAC	1050
ACAGAAATGT	AATTTTGGAA	TGAGGAATCG	AAGTTGTTCT	TCTACTTGCT	1100
GTACTTTTCT	TTTGTTTTCA	ATAAAATTTT	TACACCATAC	TGTTATCAAA	1150
CCGCCAATTA	TTGTGCACAA	TCCTCCAATG	ATTGTAGATA	AAATTGACAA	1200
TATATTACAC	ACCTTTCTTA	GAGGTTTATT	AACATCTATT	TTTGAATTTA	1250
AAATTATTAC	TTTGGTAGCG	TTATAACCTA	TTTAACAGAT	TAGAGAAAAA	1300
TTGAATGATC	GATTGAAGAA	TTTCCAAAAT	ACCGTCCCAT	ATGCGTTGAA	1350
GGAGATTTCT	ATTTTCTTCT	GTATTCAAAT	CTTTGGCTTT	ATCCTTTGCT	1400
TTATTCAATA	AATCATCTGA	GTTTTTTTCA	ATATTTTTTA	ATACATCTTT	1450
GGCATTTTGT	TTAAATACTT	TAGGATCGGA	AGTTAGGGCA	TTAGAGTTTG	1500
CCACATTAAT	CATATTATTA	TTAATCATTT	GAATTTGATT	ATCTGATAAT	1550
ATCTCTGATA	ACCTACGCTC	ATCGAGGACT	TTATTAACAG	TG	1592

2) INFORMATION FOR SEQ ID NO: 49

- (i) (A) LENGTH: 730 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: CCRI-1311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49

AGCATTTAAG	ATTATGCGTG	GAGAAGCATA	TCATAAATGA	TGCGGTTATT	50
TCAGCCGTAA	TTTTATAATA	TAAAGCAGAG	TTTATTAAAT	TTTAATGATT	100
ACTTTTTATT	AAGAATTAAT	TCTAGTTGAT	ATATTATAAT	GTGAAACACA	150
AAATAATAAT	TTGTAAATTGT	TAGTTTATAG	GCATCTGTAT	TTGGAATTTT	200
TTGTAGACTA	TTTAAAAAAT	AGTGTATATA	AGTATTGAGT	TCATGTATTA	250
ACTGTCTTTT	TTCATCGTTC	ATCAAGTATA	AGGATGTAGA	GATTTGTTGG	300
ATAATTTCTT	CGGATGTTTT	TAAAATTATC	ATTAAATTAG	ATGGTATCTG	350
ATCTTGAGTT	TTGTTTTTAG	TGTATGTATA	TTTTAAAAAA	TTTTTGATTG	400
TTGTTATTTG	ACTCTCTTTT	AATTTGACAC	CCTCATCAAT	AAATGTGTTA	450
AATATATCTT	CATTTGTACT	TAAATCATCA	AAATTTGCCA	ACAAATATTT	500
GAACGTCTCT	AAATCATTAT	GTTTGAGTTC	CGTTTTGCTA	TTCCATAATT	550
CCAAACCATT	TGGTAGAAAG	CCCAAGCTGT	GATTTTGATC	TCCCCATATA	600
GCTGAATTTA	AATCAGTGAG	TTGATTAATT	TTTTCAACAC	AGAAATGTAA	650
TTTTGGAATG	AGGAATCGAA	GTTGTTCTTC	TACTTGCTGT	ACTTTTCTTT	700
TGTTTTCAAT	AAAATTTCTA	CACCATACTG			730

2) INFORMATION FOR SEQ ID NO: 50

- (i) (A) LENGTH: 1696 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-2025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50

AAAGAGAAAT	ATTGGAAGCA	AGCCATAGCA	GAATATGAAA	AACGTTTAGG	50
CCCATACACC	AAGATAGACA	TCATAGAAGT	TCCAGACGAA	AAAGCACCAG	100
AAAATATGAG	TGACAAAGAA	ATTGAGCAAG	TAAAAGAAAA	AGAAGGCCAA	150
CGAATACTAG	CCAAAATCAA	ACCACAATCC	ACAGTCATTA	CATTAGAAAT	200
ACAAGGAAAG	ATGCTATCTT	CCGAAGGATT	AGCCCCAAGAA	TTGAACCAAC	250
GCATGACCCA	AGGGCAAAGC	GACTTTGTTT	TCGTCATTGG	CGGATCAAAÇ	300
GGCCTGCACA	AGGACGTCTT	ACAACGCAGT	AACTACGCAC	TATCATTTCAG	350
CAAAATGACA	TTCCACATC	AAATGATGCG	GGTTGTGTTA	ATTGAACAAG	400
TGTACAGAGC	ATTTAAGATT	ATGCGAGGAG	AAGCATATCA	TAAATGATGC	450
GGTTATTTCA	GCCGTAATTT	TATAATATAA	AGCAGAGTTT	ATTAAATTTT	500
AATGATTACT	TTTTATTAAG	AATTAATTCT	AGTTGATATA	TTATAATGTG	550
AAACACAAAA	TAATAATTTG	TAATTGTTAG	TTTATAGGCA	TCTGTATTTG	600
GAATTTTTTG	TAGACTATTT	AAAAAATAGT	GTATATAAGT	ATTGAGTTCA	650
TGTATTAACT	GTCTTTTTTC	ATCGTTCATC	AAGTATAAGG	ATGTAGAGAT	700
TTGTTGGATA	ATTTCTTCGG	ATGTTTTTAA	AATTATCATT	AAATTAGATG	750
GTATCTGATC	TTGAGTTTTG	TTTTTAGTGT	ATGTATAATT	TAAAAAATTT	800
TTGATTGTTG	TTATTTGACT	CTCTTTTAAT	TTGACACCCT	CATCAATAAA	850
TGTGTTAAAT	ATATCTTCAT	TTGTACTTAA	ATCATCAAAA	TTTGCCAACA	900
AATATTTGAA	CGTCTCTAAA	TCATTATGTT	TGAGTTCCGT	TTTGCTATTC	950
CATAATTCCA	AACCAATTGG	TAGAAAGCCC	AAGCTGTGAT	TTTGATCTCC	1000
CCATATAGCT	GAATTTAAAT	CAGTGAGTTG	ATTAATTTT	TCAACACAGA	1050
AATGTAATTT	TGGAATGAGG	AATCGAAGTT	GTTCTTCTAC	TTGCTGTACT	1100

TTTCTTTTGT	TTTCAATAAA	ATTTCTACAC	CATACTGTTA	TCAAACCGCC	1150
AATTATTGTG	CACAATCCTC	CAATGATTGT	AGATAAAATT	GACAATATAT	1200
TACACACCTT	TCTTAGAGGT	TTATTAACAT	CTATTTTGA	ATTTAAAATT	1250
ATTACTTTGG	TAGCGTTATA	ACCTATTTAA	CAGATTAGAG	AAAAATTGAA	1300
TGATCGATTG	AAGAATTTCC	AAAATACCGT	CCCATATGCG	TTGAAGGAGA	1350
TTTCTATTTT	CTTCTGTATT	CAATCTTTG	GCTTTATCCT	TTGCTTTATT	1400
CAATAAATCA	TCTGAGTTTT	TTTCAATATT	TTTTAATACA	TCTTTGGCAT	1450
TTTGTTTTAAA	TACTTTAGGA	TCGGAAGTTA	GGGCATTAGA	GTTTGCCACA	1500
TTAATCATAT	TATTATTAAT	CATTTGAATT	TGATTATCTG	ATAATATCTC	1550
TGATAACCTA	CGCTCATCGA	GGACTTTATT	AACAGTGTCT	TCAACTTGTT	1600
GTTGTGTGAT	TTGTTTATCT	TGATTTTGT	TAATATCTGC	AAGTTGTTCT	1650
TTAATATCTG	CTATAGAAGC	ATTTAAAGCT	TCATCTGAAT	ACCCAT	1696

2) INFORMATION FOR SEQ ID NO: 51

- (i) (A) LENGTH: 2122 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: CCRI-9504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51

GGAAACTAAA	AGAGAAATAT	TGGAAGCAAG	CCATAGCAGA	ATATGAAAAA	50
CGTTTAGGCC	CATACACCAA	GATAGACATC	ATAGAAGTTC	CAGACGAAAA	100
AGCACCAGAA	AATATGAGCG	ACAAAGAAAT	TGAGCAAGTA	AAAGAAAAAG	150
AAGGCCAACG	AATACTAGCC	AAAATCAAAC	CACAATCAAC	AGTCATTACA	200
TTAGAAATAC	AAGGAAAGAT	GCTATCTTCC	GAAGGATTGG	CCCAAGAATT	250
GAACCAACGC	ATGACCCAAG	GGCAAAGCGA	CTTTGTATTG	GTCATTGGCG	300
GATCAAACGG	CCTGCACAAG	GACGTCTTAC	AACGCAGTAA	CTACGCCTA	350
TCATTTCAGCA	AAATGACATT	CCCACATCAA	ATGATGCGGG	TTGTGTTAAT	400
TGAACAAGTG	TACAGAGCAT	TTAAGATTAT	GCGTGGAGAA	GCGTACCACA	450
AATGATGCGG	TTTTTTATCC	AGTTTTTTGT	TTAATGAACA	AGGTAAATTA	500
CGAGATAATA	TTTGAAGAAA	ACAATAAAGT	AGAGATGGAT	TTCCATATCC	550
TCTTTAGTAG	CGGTTTTTAT	CTGTAAGGTT	TATTAATAAT	TAAATAAATA	600
GGCGGGATAG	TTATATATAG	CTTATTAATG	AAAGAATATG	ATTATTAATT	650
TAGTATTATA	TTTTAATATT	AAAAAGAAGA	TATGAAATAA	TTATTCATAC	700
CTTCCACCTT	ACAATAATTA	GTTTTCAATC	GAATATTAAG	ATTATTAGTA	750
GTCTTAAAAG	TTAAGACTTC	CTTATATTAA	TGACCTAATT	TATTATTGTC	800
CTCATGAATT	ATCTTTTTAT	TTCTTTTGATA	TGTCCCAAAC	CACATCGTGA	850
TATACACTAC	AATAAATATT	ATGATGAAAC	TAATAATATT	CTCAAAGTTC	900
AGATGGAACC	AACCTGCTAG	AATAGCGAGT	GGGAAGAATA	GGATTATCAT	950
CAATATAAAG	TGAACTACAG	TCTGTTTTGT	TATACTCCAA	TCGGTATCTG	1000
TAAATATCAA	ATTACCATAA	GTAAACAAAA	TTCCAATCAA	TGCCCATAGT	1050
GCTACACATA	TTAGCATAAT	AACCGCTTCA	TTAAAGTTTT	CATAATAAAT	1100
TTTACCCATA	AAAGAATCTG	GATATAGTGG	TACATATTTA	TCCCTTGAAA	1150
AAAATAAGTG	AAGTAATGAC	AGAAATCATA	AGACCAGTGA	ACGCACCTTT	1200
TTGAACAGCG	TGGAATAATT	TTTTCTAGAT	GAGATGGACC	ATTCCATTTG	1250
TTTCTAACTT	CAAGTGATCA	ATGTAATTTA	GATTGATAAT	TTCTGATTTT	1300
GAAATACGCA	CGAATATTGA	ACCGACAAGC	TCTTCAATTT	GGTAAAGTCG	1350

CTGATAAAGT	TTTAAAGCTT	TATTATTCAT	TGTTATCGCA	TACCTGTTTA	1400
TCTTCTACTA	TGAACTGTGC	AATTTGTTCT	AGATCAATTG	GGTAAACATG	1450
ATGGTTCTGT	TGCAAAGTAA	AAAAATATAG	CTAACCACCTA	ATTTATCATG	1500
TCAGTGTTTCG	CTTAACTTGC	TAGCATGATG	CTAATTTTCGT	GGCATGGCGA	1550
AAATCCGTAAG	ATCTGATGAG	ACCTGCGGTT	CTTTTTTATAT	AGAGCGTAAA	1600
TACATTCAAT	ACCTTTTAAA	GTATTCTTTG	CTGTATTGAT	ACTTTTGATAC	1650
CTTGTCTTTC	TTACTTTAAT	ATGACGGTGA	TCTTGCTCAA	TGAGGTTATT	1700
CAGATATTTC	GATGTACAAT	GACAGTCAGG	TTTAAGTTTA	AAAGCTTTAA	1750
TTACTTTTAGC	CATTGCTACC	TTCGTTGAAG	GTGCCTGATC	TGTAATTACC	1800
TTTTGAGGTT	TACCAAATTG	TTTAATGAGA	CGTTTGATAA	ACGCATATGC	1850
TGAATGATTA	TCTCGTTGCT	TACGCAACCA	AATATCTAAT	GTATGTCCCT	1900
CTGCATCAAT	GGCACGATAT	AAATAGCTCC	ATTTTCCTTT	TATTTTGATG	1950
TACGTCTCAT	CAATACGCCA	TTTGTAATAA	GCTTTTTTTAT	GCTTTTTTCTT	2000
CCAAATTTGA	TACAAAATTG	GGGCATATTC	TTGAACCCAA	CGGTAGACCG	2050
TTGAATGATG	AACGTTTACA	CCACGTTCCC	TTAATATTTT	AGATATATCA	2100
CGATAACTCA	ATGTATATCT	TA			2122

2) INFORMATION FOR SEQ ID NO: 52

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52

GATAGACTAA TTATCTTCAT C**21**

2) INFORMATION FOR SEQ ID NO: 53

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53

CAGACTGTGG ACAAACCTGAT T**21**

2) INFORMATION FOR SEQ ID NO: 54

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54

TGAGATCATC TACATCTTTA

20

2) INFORMATION FOR SEQ ID NO: 55

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55

GGATCAAAAG CTACTAAATC

20

2) INFORMATION FOR SEQ ID NO: 56

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56

ATGCTCTTTG TTTTGCAGCA

20

2) INFORMATION FOR SEQ ID NO: 57

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57

ATGAAAGACT GCGGAGGCTA ACT

23

2) INFORMATION FOR SEQ ID NO: 58

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58

ATATTCTAGA TCATCAATAG TTG

23

2) INFORMATION FOR SEQ ID NO: 59

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59

AAGAATTGAA CCAACGCATG A

21

2) INFORMATION FOR SEQ ID NO: 60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60

GTTCAAGCCC AGAAGCGATG T**21**

2) INFORMATION FOR SEQ ID NO: 61

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61

TCGGGCATAA ATGTCAGGAA AAT**23**

2) INFORMATION FOR SEQ ID NO: 62

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62

AAACGACATG AAAATCACCA T**21**

2) INFORMATION FOR SEQ ID NO: 63

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63

TTATTAGGTA AACCAGCAGT AAGTGAACAA CCA**33**

2) INFORMATION FOR SEQ ID NO: 64

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64

GGATCAAACG GCCTGCACA**19**

2) INFORMATION FOR SEQ ID NO: 65

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65

CACAGAAATG TAATTTTGGA ATGAGG**26**

2) INFORMATION FOR SEQ ID NO: 66

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66

GTCAAAAATC ATGAACCTCA TTACTTATG**29**

2) INFORMATION FOR SEQ ID NO: 67

(i) SEQUENCE CHARACTERISTICS:

43/125

- (A) LENGTH: 29 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67

ATTCATATA TGTAATTCCT CCACATCTC

29

2) INFORMATION FOR SEQ ID NO: 68

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68

TCTACGGATT TTCGCCATGC

20

2) INFORMATION FOR SEQ ID NO: 69

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69

AACAGGTGAA TTATTAGCAC TTGTAAG

27

2) INFORMATION FOR SEQ ID NO: 70

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70

ATCAAATGAT GCGGGTTGTG T

21

2) INFORMATION FOR SEQ ID NO: 71

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71

TCATTGGCGG ATCAAACGG

19

2) INFORMATION FOR SEQ ID NO: 72

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72

ACAACGCAGT AACTACGCAC TA

22

2) INFORMATION FOR SEQ ID NO: 73

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73

TAACTACGCA CTATCATTCA GC**22**

2) INFORMATION FOR SEQ ID NO: 74

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74

ACATCAAATG ATGCGGGTTG TG**22**

2) INFORMATION FOR SEQ ID NO: 75

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75

TCAAATGATG CGGGTTGTGT TA**22**

2) INFORMATION FOR SEQ ID NO: 76

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76

CAAATGATGC GGGTTGTGTT AATT**24**

2) INFORMATION FOR SEQ ID NO: 77

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77

CTACTATGAA CTGTGCAATT TGTTCT**26**

2) INFORMATION FOR SEQ ID NO: 78

- (i) (A) LENGTH: 2007 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: NCTC 8325
- (C) ACCESSION NUMBER: Extracted from X52593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78

ATGAAAAAGA	TAAAAATTGT	TCCACTTATT	TTAATAGTTG	TAGTTGTCGG	50
GTTTGGTATA	TATTTTTTATG	CTTCAAAAGA	TAAAGAAATT	AATAATACTA	100
TTGATGCAAT	TGAAGATAAA	AATTTCAAAC	AAGTTTATAA	AGATAGCAGT	150
TATATTTCTA	AAAGCGATAA	TGGTGAAGTA	GAAATGACTG	AACGTCCGAT	200
AAAAATATAT	AATAGTTTATG	GCGTTAAAGA	TATAAACATT	CAGGATCGTA	250
AAATAAAAAA	AGTATCTAAA	AATAAAAAAC	GAGTAGATGC	TCAATATAAA	300
ATTAAAACAA	ACTACGGTAA	CATTGATCGC	AACGTTCAAT	TTAATTTTGT	350
TAAAGAAGAT	GGTATGTGGA	AGTTAGATTG	GGATCATAGC	GTCATTATTC	400
CAGGAATGCA	GAAAGACCAA	AGCATACATA	TTGAAAATTT	AAAATCAGAA	450
CGTGGTAAAA	TTTTAGACCG	AAACAATGTG	GAATTGGCCA	ATACAGGAAC	500
ACATATGAGA	TTAGGCATCG	TTCCAAAGAA	TGTATCTAAA	AAAGATTATA	550
AAGCAATCGC	TAAAGAACTA	AGTATTTCTG	AAGACTATAT	CAACAACAAA	600
TGGATCAAAA	TTGGGTACAA	GATGATACCT	TCGTTCCACT	TTAAAACCGT	650
TAAAAAAATG	GATGAATATT	TAAGTGATTT	CGCAAAAAAA	TTTCATCTTA	700
CAACTAATGA	AACAGAAAGT	CGTAACTATC	CTCTAGAAAA	AGCGACTTCA	750
CATCTATTAG	GTTATGTTGG	TCCCATTAAC	TCTGAAGAAT	TAAAACAAAA	800
AGAATATAAA	GGCTATAAAG	ATGATGCAGT	TATTGGTAAA	AAGGGACTCG	850
AAAAACTTTA	CGATAAAAAG	CTCCAACATG	AAGATGGCTA	TCGTGTCACA	900
ATCGTTGACG	ATAATAGCAA	TACAATCGCA	CATACATTAA	TAGAGAAAAA	950

GAAAAAAGAT	GGCAAAGATA	TTCAACTAAC	TATTGATGCT	AAAGTTCAAA	1000
AGAGTATTTA	TAACAACATG	AAAAATGATT	ATGGCTCAGG	TACTGCTATC	1050
CACCCTCAAA	CAGGTGAATT	ATTAGCACTT	GTAAGCACAC	CTTCATATGA	1100
CGTCTATCCA	TTTATGTATG	GCATGAGTAA	CGAAGAATAT	AATAAATTAA	1150
CCGAAGATAA	AAAAGAACCT	CTGCTCAACA	AGTTCCAGAT	TACAACTTCA	1200
CCAGGTTCAA	CTCAAAAAAT	ATTAACAGCA	ATGATTGGGT	TAAATAACAA	1250
AACATTAGAC	GATAAAACAA	GTTATAAAAT	CGATGGTAAA	GGTTGGCAAA	1300
AAGATAAATC	TTGGGGTGGT	TACAACGTTA	CAAGATATGA	AGTGGTAAAT	1350
GGTAATATCG	ACTTAAACAA	AGCAATAGAA	TCATCAGATA	ACATTTTCTT	1400
TGCTAGAGTA	GCACTCGAAT	TAGGCAGTAA	GAAATTTGAA	AAAGGCATGA	1450
AAAAACTAGG	TGTTGGTGAA	GATATACCAA	GTGATTATCC	ATTTTATAAT	1500
GCTCAAATTT	CAAACAAAAA	TTTAGATAAT	GAAATATTAT	TAGCTGATTC	1550
AGGTTACGGA	CAAGGTGAAA	TACTGATTAA	CCCAGTACAG	ATCCTTTCAA	1600
TCTATAGCGC	ATTAGAAAAT	AATGGCAATA	TTAACGCACC	TCACTTATTA	1650
AAAGACACGA	AAAACAAAGT	TTGGAAGAAA	AATATTATTT	CCAAAGAAAA	1700
TATCAATCTA	TTAAATGATG	GTATGCAACA	AGTCGTAAAT	AAAACACATA	1750
AAGAAGATAT	TTATAGATCT	TATGCAAAC	TAATTGGCAA	ATCCGGTACT	1800
GCAGAACTCA	AAATGAAACA	AGGAGAAAGT	GGCAGACAAA	TTGGGTGGTT	1850
TATATCATAT	GATAAAGATA	ATCCAAACAT	GATGATGGCT	ATTAATGTTA	1900
AAGATGTACA	AGATAAAGGA	ATGGCTAGCT	ACAATGCCAA	AATCTCAGGT	1950
AAAGTGTATG	ATGAGCTATA	TGAGAACGGT	AATAAAAAAT	ACGATATAGA	2000
TGAATAA					2007

2) INFORMATION FOR SEQ ID NO: 79

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79

CAAATATTAT CTCGTAATTT ACCTTGTTT**29**

2) INFORMATION FOR SEQ ID NO: 80

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80

CTCTGCTTTA TATTATAAAA TTACGGCTG**29**

2) INFORMATION FOR SEQ ID NO: 81

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81

ATTGCTGTGA ATATTTTTTG AGTTGAA**27**

2) INFORMATION FOR SEQ ID NO: 82

- (i) (A) LENGTH: 2007 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: NCTC 10442
- (C) ACCESSION NUMBER: Extracted from AB033763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82

ATGAAAAAGA	TAAAAATTGT	TCCACTTATT	TTAATAGTTG	TAGTTGTCGG	50
GTTTGGTATA	TATTTTTTATG	CTTCAAAAGA	TAAAGAAATT	AATAATACTA	100
TTGATGCAAT	TGAAGATAAA	AATTTCAAAC	AAGTTTATAA	AGATAGCAGT	150
TATATTTCTA	AAAGCGATAA	TGGTGAAGTA	GAAATGACTG	AACGTCCGAT	200
AAAAATATAT	AATAGTTTAG	GCGTTAAAGA	TATAAACATT	CAGGATCGTA	250
AAATAAAAAA	AGTATCTAAA	AATAAAAAAC	GAGTAGATGC	TCAATATAAA	300
ATTAAAACAA	ACTACGGTAA	CATTGATCGC	AACGTTCAAT	TTAATTTTGT	350
TAAAGAAGAT	GGTATGTGGA	AGTTAGATTG	GGATCATAGC	GTCATTATTC	400
CAGGAATGCA	GAAAGACCAA	AGCATACATA	TTGAAAATTT	AAAATCAGAA	450
CGTGGTAAAA	TTTGTAGACCG	AAACAATGTG	GAATTGGCCA	ATACAGGAAC	500
AGCATATGAG	ATAGGCATCG	TTCCAAAGAA	TGTATCTAAA	AAAGATTATA	550
AAGCAATCGC	TAAAGAACTA	AGTATTTCTG	AAGACTATAT	CAAACAACAA	600
ATGGATCAAA	ATTGGGTACA	AGATGATACC	TTCGTTCCAC	TTAAAACCGT	650
TAAAAAAATG	GATGAATATT	TAAGTGATTT	CGCAAAAAAA	TTTCATCTTA	700
CAACTAATGA	AACAGAAAGT	CGTAACTATC	CTCTAGAAAA	AGCGACTTCA	750

CATCTATTAG	GTTATGTTGG	TCCCATTAAC	TCTGAAGAAT	TAAAACAAAA	800
AGAATATAAA	GGCTATAAAG	ATGATGCAGT	TATTGGTAAA	AAGGGACTCG	850
AAAAACTTTA	CGATAAAAAG	CTCCAACATG	AAGATGGCTA	TCGTGTCACA	900
ATCGTTGACG	ATAATAGCAA	TACAATCGCA	CATACATTAA	TAGAGAAAAA	950
GAAAAAAGAT	GGCAAAGATA	TTCAACTAAC	TATTGATGCT	AAAGTTCAAA	1000
AGAGTATTTA	TAACAACATG	AAAAATGATT	ATGGCTCAGG	TACTGCTATC	1050
CACCCTCAAA	CAGGTGAATT	ATTAGCACTT	GTAAGCACAC	CTTCATATGA	1100
CGTCTATCCA	TTTATGTATG	GCATGAGTAA	CGAAGAATAT	AATAAATTAA	1150
CCGAAGATAA	AAAAGAACCT	CTGCTCAACA	AGTTCCAGAT	TACAAC TTCA	1200
CCAGGTTCAA	CTCAAAAAAT	ATTAACAGCA	ATGATTGGGT	TAAATAACAA	1250
AACATTAGAC	GATAAAACAA	GTTATAAAAT	CGATGGTAAA	GGTTGGCAAA	1300
AAGATAAATC	TTGGGGTGGT	TACAACGTTA	CAAGATATGA	AGTGGTAAAT	1350
GGTAATATCG	ACTTAAACAA	AGCAATAGAA	TCATCAGATÀ	ACATTTTCTT	1400
TGCTAGAGTA	GCACTCGAAT	TAGGCAGTAA	GAAATTTGAA	AAAGGCATGA	1450
AAAACTAGG	TGTTGGTGAA	GATATACCAA	GTGATTATCC	ATTTTATAAT	1500
GCTCAAATTT	CAAACAAAAA	TTTAGATAAT	GAAATATTAT	TAGCTGATTC	1550
AGGTTACGGA	CAAGGTGAAA	TACTGATTAA	CCCAGTACAG	ATCCTTTCAA	1600
TCTATAGCGC	ATTAGAAAAT	AATGGCAATA	TTAACGCACC	TCACTTATTA	1650
AAAGACACGA	AAAACAAAGT	TTGGAAGAAA	AATATTATTT	CCAAAGAAAA	1700
TATCAATCTA	TTAACTGATG	GTATGCAACA	AGTCGTAAAT	AAAACACATA	1750
AAGAAGATAT	TTATAGATCT	TATGCAAAC	TAATTGGCAA	ATCCGGTACT	1800
GCAGAACTCA	AAATGAAACA	AGGAGAAACT	GGCAGACAAA	TTGGGTGGTT	1850
TATATCATAT	GATAAAGATA	ATCCAAACAT	GATGATGGCT	ATTAATGTTA	1900
AAGATGTACA	AGATAAAGGA	ATGGCTAGCT	ACAATGCCAA	AATCTCAGGT	1950
AAAGTGTATG	ATGAGCTATA	TGAGAACGGT	AATAAAAAAT	ACGATATAGA	2000
TGAATAA					2007

2) INFORMATION FOR SEQ ID NO: 83

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83

CCCACCCAC ATCAAATGAT GCGGGTTGTG GGTGGG

36

2) INFORMATION FOR SEQ ID NO: 84

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84

CCCGCGCGTA GTTACTGCGT TGTAAGACGT CCGCGGG

37

2) INFORMATION FOR SEQ ID NO: 85

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85

GTTTTTATCA CCATATTGAA TTTATAC

27

2) INFORMATION FOR SEQ ID NO: 86

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86

ATTACTTGA AAGACTGCGG AGGAG

25

2) INFORMATION FOR SEQ ID NO: 87

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87

TGTTTGAGCT TCCACAGCTA TTTC**24**

2) INFORMATION FOR SEQ ID NO: 88

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88

CCCTATAATT CCAATTATTG CACTAAC**27**

2) INFORMATION FOR SEQ ID NO: 89

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89

ATGAGGAGAT AATAATTG AGGGT**25**

2) INFORMATION FOR SEQ ID NO: 90

(i) (A) LENGTH: 2007 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: N315
- (C) ACCESSION NUMBER: Extracted from D86934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90

ATGAAAAAGA	TAAAAATTGT	TCCACTTATT	TTAATAGTTG	TAGTTGTCGG	50
GTTTGGTATA	TATTTTTTATG	CTTCCAAAGA	TAAAGAAATT	AATAATACTA	100
TTGATGCAAT	TGAAGATAAA	AATTTCAAAC	AAGTTTATAA	AGATAGCAGT	150
TATATTTCTA	AAAGCGATAA	TGGTGAAGTA	GAAATGACTG	AACGTCCGAT	200
AAAAATATAT	AATAGTTTATG	GCGTTAAAGA	TATAAACATT	CAGGATCGTA	250
AAATAAAAAA	AGTATCTAAA	AATAAAAAAC	GAGTAGATGC	TCAATATAAA	300
ATTAAAACAA	ACTACGGTAA	CATTGATCGC	AACGTTCAAT	TTAATTTTGT	350
TAAAGAAGAT	GGTATGTGGA	AGTTAGATTG	GGATCATAGC	GTCATTATTC	400
CAGGAATGCA	GAAAGACCAA	AGCATACATA	TTGAAAATTT	AAAATCAGAA	450
CGTGGTAAAA	TTTTAGACCG	AAACAATGTG	GAATTGGCCA	ATACAGGAAC	500
AGCATATGAG	ATAGGCATCG	TTCCAAAGAA	TGTATCTAAA	AAAGATTATA	550
AAGCAATCGC	TAAAGAACTA	AGTATTTCTG	AAGACTATAT	CAAACAACAA	600
ATGGATCAAA	ATTGGGTACA	AGATGATACC	TTCGTTCCAC	TTAAAACCGT	650
TAAAAAAATG	GATGAATATT	TAAGTGATTT	CGCAAAAAAA	TTTCATCTTA	700
CAACTAATGA	AACAGAAAGT	CGTAACTATC	CTCTAGGAAA	AGCGACTTCA	750
CATCTATTAG	GTTATGTTGG	TCCCATTAAC	TCTGAAGAAT	TAAAACAAAA	800
AGAATATAAA	GGCTATAAAG	ATGATGCAGT	TATTGGTAAA	AAGGGACTCG	850
AAAAACTTTA	CGATAAAAAG	CTCCAACATG	AAGATGGCTA	TCGTGTCACA	900
ATCGTTGACG	ATAATAGCAA	TACAATCGCA	CATACATTAA	TAGAGAAAAA	950
GAAAAAAGAT	GGCAAAGATA	TTCAACTAAC	TATTGATGCT	AAAGTTCAAA	1000
AGAGTATTTA	TAACAACATG	AAAAATGATT	ATGGCTCAGG	TACTGCTATC	1050
CACCCTCAAA	CAGGTGAATT	ATTAGCACTT	GTAAGCACAC	CTTCATATGA	1100
CGTCTATCCA	TTTATGTATG	GCATGAGTAA	CGAAGAATAT	AATAAATTAA	1150
CCGAAGATAA	AAAAGAACCT	CTGCTCAACA	AGTTCAGAT	TACAACTTCA	1200
CCAGGTTCAA	CTCAAAAAAT	ATTAACAGCA	ATGATTGGGT	TAAATAACAA	1250
AACATTAGAC	GATAAAACAA	GTTATAAAAT	CGATGGTAAA	GGTTGGCAAA	1300
AAGATAAATC	TTGGGGTGGT	TACAACGTTA	CAAGATATGA	AGTGGTAAAT	1350
GGTAATATCG	ACTTAAACAA	AGCAATAGAA	TCATCAGATA	ACATTTTCTT	1400
TGCTAGAGTA	GCACTCGAAT	TAGGCAGTAA	GAAATTTGAA	AAAGGCATGA	1450
AAAAACTAGG	TGTTGGTGAA	GATATACCAA	GTGATTATCC	ATTTTATAAT	1500
GCTCAAATTT	CAAACAAAAA	TTTAGATAAT	GAAATATTAT	TAGCTGATTC	1550
AGGTTACGGA	CAAGGTGAAA	TACTGATTAA	CCCAGTACAG	ATCCTTTCAA	1600
TCTATAGCGC	ATTAGAAAAT	AATGGCAATA	TTAACGCACC	TCACTTATTA	1650
AAAGACACGA	AAAACAAAGT	TTGGAAGAAA	AATATTATTT	CCAAAGAAAA	1700
TATCAATCTA	TTAACTGATG	GTATGCAACA	AGTCGTAAAT	AAAACACATA	1750
AAGAAGATAT	TTATAGATCT	TATGCAAAC	TAATTGGCAA	ATCCGGTACT	1800
GCAGAACTCA	AAATGAAACA	AGGAGAAACT	GGCAGACAAA	TTGGGTGGTT	1850
TATATCATAT	GATAAAGATA	ATCCAAACAT	GATGATGGCT	ATTAATGTTA	1900
AAGATGTACA	AGATAAAGGA	ATGGCTAGCT	ACAATGCCAA	AATCTCAGGT	1950
AAAGTGTATG	ATGAGCTATA	TGAGAACGGT	AATAAAAAAT	ACGATATAGA	2000
TGAATAA					2007

2) INFORMATION FOR SEQ ID NO: 91

- (i) (A) LENGTH: 2007 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

(B) STRAIN: 85/2082

(C) ACCESSION NUMBER: Extracted from AB037671

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91

ATGAAAAAGA	TAAAAATTGT	TCCACTTATT	TTAATAGTTG	TAGTTGTCGG	50
GTTTGGTATA	TATTTTTTATG	CTTCAAAAGA	TAAAGAAATT	AATAATACTA	100
TTGATGCAAT	TGAAGATAAA	AATTTCAAAC	AAGTTTATAA	AGATAGCAGT	150
TATATTTCTA	AAAGCGATAA	TGGTGAAGTA	GAAATGACTG	AACGTCCGAT	200
AAAAATATAT	AATAGTTTAG	GCGTTAAAGA	TATAAACATT	CAGGATCGTA	250
AAATAAAAAA	AGTATCTAAA	AATAAAAAAC	GAGTAGATGC	TCAATATAAA	300
ATTAAACAA	ACTACGGTAA	CATTGATCGC	AACGTTCAAT	TTAATTTTGT	350
TAAAGAAGAT	GGTATGTGGA	AGTTAGATTG	GGATCATAGC	GTCATTATTC	400
CAGGAATGCA	GAAAGACCAA	AGCATACATA	TTGAAAATTT	AAAATCAGAA	450
CGTGGTAAAA	TTTTAGACCG	AAACAATGTG	GAATTGGCCA	ATACAGGAAC	500
AGCATATGAG	ATAGGCATCG	TTCCAAAGAA	TGTATCTAAA	AAAGATTATA	550
AAGCAATCGC	TAAAGAACTA	AGTATTTCTG	AAGACTATAT	CAAACAACAA	600
ATGGATCAAA	AGTGGGTACA	AGATGATACC	TTCGTTCCAC	TTAAAACCGT	650
TAAAAAAATG	GATGAATATT	TAAGTGATTT	CGCAAAAAAA	TTTCATCTTA	700
CAACTAATGA	AACAGAAAGT	CGTAACTATC	CTCTAGAAAA	AGCGACTTCA	750
CATCTATTAG	GTTATGTTGG	TCCCATTAAAC	TCTGAAGAAT	TAAAACAAAA	800
AGAATATAAA	GGCTATAAAG	ATGATGCAGT	TATTGGTAAA	AAGGGACTCG	850
AAAAACTTTA	CGATAAAAAG	CTCCAACATG	AAGATGGCTA	TCGTGTCACA	900
ATCGTTGACG	ATAATAGCAA	TACAATCGCA	CATACATTAA	TAGAGAAAAA	950
GAAAAAAGAT	GGCAAAGATA	TTCAACTAAC	TATTGATGCT	AAAGTTCAAA	1000
AGAGTATTTA	TAACAACATG	AAAAATGATT	ATGGCTCAGG	TACTGCTATC	1050
CACCCTCAAA	CAGGTGAATT	ATTAGCACTT	GTAAGCACAC	CTTCATATGA	1100
CGTCTATCCA	TTTATGTATG	GCATGAGTAA	CGAAGAATAT	AATAAATTAA	1150
CCGAAGATAA	AAAAGAACCT	CTGCTCAACA	AGTTCCAGAT	TACAACTTCA	1200
CCAGGTTCAA	CTCAAAAAAT	ATTAACAGCA	ATGATTGGGT	TAAATAACAA	1250
AACATTAGAC	GATAAAACAA	GTTATAAAAT	CGATGGTAAA	GGTTGGCAAA	1300
AAGATAAATC	TTGGGGTGGT	TACAACGTTA	CAAGATATGA	AGTGGTAAAT	1350
GGTAATATCG	ACTTAAACAA	AGCAATAGAA	TCATCAGATA	ACATTTTCTT	1400
TGCTAGAGTA	GCACTCGAAT	TAGGCAGTAA	GAAATTTGAA	AAAGGCATGA	1450
AAAAACTAGG	TGTTGGTGAA	GATATACCAA	GTGATTATCC	ATTTTATAAT	1500
GCTCAAATTT	CAAACAAAAA	TTTAGATAAT	GAAATATTAT	TAGCTGATTC	1550
AGGTTACGGA	CAAGGTGAAA	TACTGATTAA	CCCAGTACAG	ATCCTTTCAA	1600
TCTATAGCGC	ATTAGAAAAT	AATGGCAATA	TTAACGCACC	TCACTTATTA	1650
AAAGACACGA	AAAACAAAGT	TTGGAAGAAA	AATATTATTT	CCAAAGAAAA	1700
TATCAATCTA	TTAACTGATG	GTATGCAACA	AGTCGTAAAT	AAAACACATA	1750
AAGAAGATAT	TTATAGATCT	TATGCAAAC	TAATTGGCAA	ATCCGGTACT	1800
GCAGAACTCA	AAATGAAACA	AGGAGAACT	GGCAGACAAA	TTGGGTGGTT	1850
TATATCATAT	GATAAAGATA	ATCCAAACAT	GATGATGGCT	ATTAATGTTA	1900
AAGATGTACA	AGATAAAGGA	ATGGCTAGCT	ACAATGCCAA	AATCTCAGGT	1950
AAAGTGTATG	ATGAGCTATA	TGAGAACGGT	AATAAAAAAT	ACGATATAGA	2000
TGAATAA					2007

2) INFORMATION FOR SEQ ID NO: 92

- (i) (A) LENGTH: 675 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: NCTC 10442
- (C) ACCESSION NUMBER: Extracted from AB033763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92

ATGAACTATT	TCAGATATAA	ACAATTTAAC	AAGGATGTTA	TCACTGTAGC	50
CGTTGGCTAC	TATCTAAGAT	ATACATTGAG	TTATCGTGAT	ATATCTGAAA	100
TATTAAGGGA	ACGTGGTGTA	AACGTTTCATC	ATTCAACGGT	CTACCGTTGG	150
GTTCAAGAAT	ATGCCCCAAT	TTTGTATCAA	ATTTGGAAGA	AAAAGCATAA	200
AAAAGCTTAT	TACAAATGGC	GTATTGATGA	GACGTACATC	AAAATAAAAG	250
GAAAATGGAG	CTATTTATAT	CGTGCCATTG	ATGCAGAGGG	ACATACATTA	300
GATATTTGGT	TGCGTAAGCA	ACGAGATAAT	CATTCAGCAT	ATGCGTTTAT	350
CAAACGTCTC	ATTAAACAAT	TTGGTAAACC	TCAAAAGGTA	ATTACAGATC	400
AGGCACCTTC	AACGAAGGTA	GCAATGGCTA	AAGTAATTAA	AGCTTTTAAA	450
CTTAAACCTG	ACTGTCATTG	TACATCGAAA	TATCTGAATA	ACCTCATTGA	500
GCAAGATCAC	CGTCATATTA	AAGTAAGAAA	GACAAGGTAT	CAAAGTATCA	550
ATACAGCAAA	GAATACTTTA	AAAGGTATTG	AATGTATTTA	CGCTCTATAT	600
AAAAAGAACC	GCAGGTCTCT	TCAGATCTAC	GGATTTTCGC	CATGCCACGA	650
AATTAGCATC	ATGCTAGCAA	GTTAA			675

2) INFORMATION FOR SEQ ID NO: 93

- (i) (A) LENGTH: 675 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: N315
- (C) ACCESSION NUMBER: Extracted from D86934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93

ATGAACTATT	TCAGATATAA	ACAATTTAAC	AAGGATGTTA	TCACTGTAGC	50
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CGTTGGCTAC	TATCTAAGAT	ATACATTGAG	TTATCGTGAT	ATATCTGAAA	100
TATTAAGGGA	ACGTGGTGTA	AACGTTTCATC	ATTCAACGGT	CTACCGTTGG	150
GTTCAAGAAT	ATGCCCCAAT	TTTGTATCAA	ATTTGGAAGA	AAAAGCATAA	200
AAAAGCTTAT	TACAAATGGC	GTATTGATGA	GACGTACATC	AAAATAAAAAG	250
GAAAATGGAG	CTATTTATAT	CGTGCCATTG	ATGCAGAGGG	ACATACATTA	300
GATATTTGGT	TGCGTAAGCA	ACGAGATAAT	CATTCAGCAT	ATGCGTTTAT	350
CAAACGTCTC	ATTAAACAAT	TTGGTAAACC	TCAAAAGGTA	ATTACAGATC	400
AGGCACCTTC	AACGAAGGTA	GCAATGGCTA	AAGTAATTAA	AGCTTTTAAA	450
CTTAAACCTG	ACTGTCATTG	TACATCGAAA	TATCTGAATA	ACCTCATTGA	500
GCAAGATCAC	CGTCATATTA	AAGTAAGAAA	GACAAGGTAT	CAAAGTATCA	550
ATACAGCAAA	GAATACTTTA	AAAGGTATTG	AATGTATTTA	CGCTCTATAT	600
AAAAAGAACC	GCAGGTCTCT	TCAGATCTAC	GGATTTTCGC	CATGCCACGA	650
AATTAGCATC	ATGCTAGCAA	GTTAA			675

2) INFORMATION FOR SEQ ID NO: 94

- (i) (A) LENGTH: 675 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: HUC19
- (C) ACCESSION NUMBER: Extracted from AF181950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94

ATGAACTATT	TCAGATATAA	ACAATTTAAC	AAGGATGTTA	TCACTGTAGC	50
CGTTGGCTAC	TATCTAAGAT	ATACATTGAG	TTATCGTGAT	ATATCTGAAA	100
TATTAAGGGA	ACGTGGTGTA	AACGTTTCATC	ATTCAACGGT	CTACCGTTGG	150
GTTCAAGAAT	ATGCCCCAAT	TTTGTATCAA	ATTTGGAAGA	AAAAGCATAA	200
AAAAGCTTAT	TACAAATGGC	GTATTGATGA	GACGTACATC	AAAATAAAAAG	250
GAAAATGGAG	CTATTTATAT	CGTGCCATTG	ATGCAGAGGG	ACATACATTA	300
GATATTTGGT	TGCGTAAGCA	ACGAGTTAAT	CATTCAGCAT	ATGCGTTTAT	350
CAAACGTCTC	ATTAAACAAT	TTGGTAAACC	TCAAAAGGTA	ATTACAGATC	400
AGGCACCTTC	AACGAAGGTA	GCAATGGCTA	AAGTAATTAA	AGCTTTTAAA	450
CTTAAACCTG	ACTGTCATTG	TACATCGAAA	TATCTGAATA	ACCTCATTGA	500
GCAAGATCAC	CGTCATATTA	AAGTAAGAAA	GACAAGGTAT	CAAAGTATCA	550
ATACAGCAAA	GAATACTTTA	AAAGGTATTG	AATGTATTTA	CGCTCTATAT	600
AAAAAGAACC	GCAGGTCTCT	TCAGATCTAC	GGATTTTCGC	CATGCCACGA	650
AATTAGCATC	ATGCTAGCAA	GTTAA			675

2) INFORMATION FOR SEQ ID NO: 95

- (i) (A) LENGTH: 675 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: NCTC 8325
- (C) ACCESSION NUMBER: Extracted from X53818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95

ATGAACTATT	TCAGATATAA	ACAATTTAAC	AAGGATGTTA	TCACTGTAGC	50
CGTTGGCTAC	TATCTAAGAT	ATACATTGAG	TTATCGTGAT	ATATCTGAAA	100
TATTAAGGGA	ACGTGGTGTA	AACGTTTCATC	ATTCAACGGT	CTACCGTTGG	150
GTTCAAGAAT	ATGCCCCAAT	TTTGTATCAA	ATTTGGAAGA	AAAAGCATAA	200
AAAAGCTTAT	TACAAATGGC	GTATTGATGA	GACGTACATC	AAAATAAAAG	250
GAAAATGGAG	CTATTTTATAT	CGTGCCATTG	ATGCAGAGGG	ACATACATTA	300
GATATTTGGT	TGCGTAAGCA	ACGAGATAAT	CATTCAGCAT	ATGCGTTTAT	350
CAAACGTCTC	ATTAAACAAT	TTGGTAAACC	TCAAAAGGTA	ATTACAGATC	400
AGGCACCTTC	AACGAAGGTA	GCAATGGCTA	AAGTAATTAA	AGCTTTTAAA	450
CTTAAACCTG	ACTGTCATTG	TACATCGAAA	TATCTGAATA	ACCTCATTGA	500
GCAAGATCAC	CGTCATATTA	AAGTAAGAAA	GACAAGGTAT	CAAAGTATCA	550
ATACAGCAAA	GAATACTTTA	AAAGGTATTG	AATGTATTTA	CGCTCTATAT	600
AAAAAGAACC	GCAGGTCTCT	TCAGATCTAC	GGATTTTCGC	CATGCCACGA	650
AATTAGCATC	ATGCTAGCAA	GTTAA			675

2) INFORMATION FOR SEQ ID NO: 96

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96

GTAAAGTGTA TGATGAGCTA TATGAGAA

28

2) INFORMATION FOR SEQ ID NO: 97

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

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(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97

GCTGAAAAAA CCGCATCATT TRTGRTA

27

2) INFORMATION FOR SEQ ID NO: 98

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98

TTTAGTTTTA TTTATGATAC GCTTCTCCA

29

2) INFORMATION FOR SEQ ID NO: 99

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99

GCTGAAAAAA CCGCATCATT TATGATA

27

2) INFORMATION FOR SEQ ID NO: 100

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100

CTATGTCAAA AATCATGAAC CTCATTAC

28

2) INFORMATION FOR SEQ ID NO: 101

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101

GGAGGCTAAC TATGTCAAAA ATC

23

2) INFORMATION FOR SEQ ID NO: 102

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102

CTCTATAAAC ATCGTATGAT ATTGC

25

2) INFORMATION FOR SEQ ID NO: 103

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103

ACCAAACGAC ATGAAAATCA

20

2) INFORMATION FOR SEQ ID NO: 104

- (i) (A) LENGTH: 1256 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
 (B) STRAIN: 85/2082
 (C) ACCESSION NUMBER: Extracted from AB037671

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104

TTCAGAAAAA	TGATTAATGT	GTTTCAATAA	AATCTCTCCT	TCTTTGTGAA	50
CATATTCATT	TTTATACTAA	TTAATATAAT	TTCCAAAAAA	GTTTCTGTTT	100
AAAAGTGAAA	AATATTATTT	ACCGTTTGAC	TTAAATCTTC	AATATATAGG	150
TGTTTATATG	TATCATTTTG	CGCCAATTTG	AATAAACGGG	AATCAAGTCT	200
GTTTCTGAGT	TTATTTCAAC	TTTCTTATAG	TAAACATTGT	CTTAATATGA	250
TGAACCTCAA	TAAAACTTTC	CCTATGCCCC	ATAAAATTTT	CTCAAAATCA	300
AAAATAACAT	ACCTTACAAC	TTTTACCGTC	GATATCAATT	GCTCTTTTCT	350
TAATTTAGGA	TTGCTTTCAA	ATTTTGTACT	ATAACGTGAA	ACTACTTTTC	400
CTTCTTTATA	ATTAAAATTT	ACTAATTCAC	AATCATTTTT	ACTTCCATTT	450
ACAAAAACAT	CCACTGTTTC	TAACACAAAA	TCTAATAAAC	TTCCTTTTAT	500
TAATCGTAGG	CATTGTATAT	TTCCTTTTCAT	TCTTTCTTGA	TTCCATTAGT	550
TTAAATTTAA	AATTTTCATCC	ATCAATTTCT	TAATTTAATT	GTAGTTCCAT	600
AATCAATATA	ATTTGTACAG	TTATTATATA	TTCTAGATCA	TCAATAGTTG	650
AAAAATGGTT	TATTAAACAC	TCTATAAACA	TCGTATGATA	TTGCAAGGTA	700
TAATCCAATA	TTTCATATAT	GTAATTCCTC	CACATCTCAT	TAAATTTTTA	750
AATTATACAC	AACCTAATTT	TTAGTTTTAT	TTATGATACG	CTTCTCCACG	800
CATAATCTTA	AATGCTCTGT	ACACTTGTTT	AATTAACACA	ACCCGCATCA	850
TTTGATGTGG	GAATGTCATT	TTGCTGAATG	ATAGTGCGTA	GTTACTGCGT	900
TGTAAGACGT	CCTTGTGCAG	GCCGTTTGAT	CCGCCAATGA	CGAATACAAA	950
GTCGCTTTGC	CCTTGGGTCA	TGCGTTGGTT	CAATTCTTGG	GCCAATCCTT	1000
CGGAAGATAG	CATCTTTCCT	TGTATTTCTA	ATGTAATGAC	TGTTGATTGT	1050
GGTTTGATTT	TGGCTAGTAT	TCGTTGGCCT	TCTTTTTCTT	TTACTTGCTC	1100
AATTTCTTTG	TCGCTCATAT	TTTCTGGTGC	TTTTTCGTCT	GGAACCTCTA	1150
TGATGTCTAT	CTTGGTGTAT	GGGCCTAAAC	GTTTTTCATA	TTCTGCTATG	1200
GCTTGCTTCC	AATATTTCTC	TTTTAGTTTC	CCTACAGCTA	AAATGGTGAT	1250
TTTCAT					1256

2) INFORMATION FOR SEQ ID NO: 105

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105

TCATGAACCT CATTACTTAT GATAAGIT

28

2) INFORMATION FOR SEQ ID NO: 106

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106

GAAAAAACCG CATCATTTAT GATATGIT

28

2) INFORMATION FOR SEQ ID NO: 107

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107

CCTAATTTTT AGTTTTATTT ATGATACGIT

30

2) INFORMATION FOR SEQ ID NO: 108

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108

CACAACCTAA TTTTGTAGTTT TATTTATGAT ACGIT

35

2) INFORMATION FOR SEQ ID NO: 109

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109

TGATAAGCCA TTCATTCACC CTAA

24

2) INFORMATION FOR SEQ ID NO: 110

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110

AAGGACTCCT AATTTATGTC TAATTCC

27

2) INFORMATION FOR SEQ ID NO: 111

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111

ATGGGAGTCC TTCGCTATTC TGTG

24

2) INFORMATION FOR SEQ ID NO: 112

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- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112

CACTTTTTAT TCTTCAAAGA TTGAGC

27

2) INFORMATION FOR SEQ ID NO: 113

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113

ATGGAAATTC TTAATCTTTA CTTGTACC

28

2) INFORMATION FOR SEQ ID NO: 114

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114

AGCATCTTCT TTACATCGCT TACT

24

2) INFORMATION FOR SEQ ID NO: 115

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 bases
(B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115

CAGCAATTCW CATAAACCTC ATA

23

2) INFORMATION FOR SEQ ID NO: 116

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116

ACAAACTTTG AGGGGATTTT TAGTAAA

27

2) INFORMATION FOR SEQ ID NO: 117

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117

TATATTGTGG CATGATTCT TC

22

2) INFORMATION FOR SEQ ID NO: 118

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118
CGAATGGACT AGCACTTTCT AAA 23

2) INFORMATION FOR SEQ ID NO: 119

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119
TTGAGGATCA AAAGTTGTTG C 21

2) INFORMATION FOR SEQ ID NO: 120

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120
CGATGATTTT ATAGTAGGAG A 21

2) INFORMATION FOR SEQ ID NO: 121

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121
TTCAATCTCT AAATCTAAAT CAGTTTGT 28

2) INFORMATION FOR SEQ ID NO: 122

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122

AGGCGAGAAA ATGGAACATA TCAA

24

2) INFORMATION FOR SEQ ID NO: 123

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123

GGTACAAGTA AAGATTAAGA ATTTCC

26

2) INFORMATION FOR SEQ ID NO: 124

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124

AGACAACTTT ATGCAGGTCC TT

22

2) INFORMATION FOR SEQ ID NO: 125

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125

TAACTGCTTG GGTAACCTTA TC

22

2) INFORMATION FOR SEQ ID NO: 126

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126

TATTGCAGGT TTCGATGTTG A

21

2) INFORMATION FOR SEQ ID NO: 127

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127

TGACCCATAT CGCCTAAAAT AC

22

2) INFORMATION FOR SEQ ID NO: 128

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128

AAAGGACAAC AAGGTAGCAA AG

22

2) INFORMATION FOR SEQ ID NO: 129

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129

TCTGTGGATA AACACCTTGA TG

22

2) INFORMATION FOR SEQ ID NO: 130

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130

GTTTGATCCG CCAATGAC

18

2) INFORMATION FOR SEQ ID NO: 131

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131

GGCATAAATG TCAGGAAAAT ATC

23

2) INFORMATION FOR SEQ ID NO: 132

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132

GAGGACCAAA CGACATGAAA ATC

23

2) INFORMATION FOR SEQ ID NO: 133

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133

TTCGAGGTTG ATGGGAAGCA

20

2) INFORMATION FOR SEQ ID NO: 134

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134

CGCTCGACTC AGGGTGTT

18

2) INFORMATION FOR SEQ ID NO: 135

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135

CGTTGAAGAT GCCTTTGA

18

2) INFORMATION FOR SEQ ID NO: 136

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136

TTTTGCAACA GCCATTCG

18

2) INFORMATION FOR SEQ ID NO: 137

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137

GCACACATGT TGTAAGTTTG C

21

2) INFORMATION FOR SEQ ID NO: 138

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138

ACGCAAACCTT ACAACATGTG TG

22

2) INFORMATION FOR SEQ ID NO: 139

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139

CGTTTGTCTG ATTTGGAGGA AG

22

2) INFORMATION FOR SEQ ID NO: 140

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140

TTTCTTCATC ATCGGTCATA AAAT

24

2) INFORMATION FOR SEQ ID NO: 141

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141

CTACGTGAAT CAAAACAAT GGA

23

2) INFORMATION FOR SEQ ID NO: 142

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142

TACTGCAAAG TCTCGTTCAT CC

22

2) INFORMATION FOR SEQ ID NO: 143

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143

CATACCATTT TGAACGATGA CCTC

24

2) INFORMATION FOR SEQ ID NO: 144

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144

ATGTCTGGTC AACTTTCCGA CTC

23

2) INFORMATION FOR SEQ ID NO: 145

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145

CAATCGGTAT CTGTAAATAT CAAAT

25

2) INFORMATION FOR SEQ ID NO: 146

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146

TCGCATACCT GTTTATCTTC TACT

24

2) INFORMATION FOR SEQ ID NO: 147

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147

TTGGTTCCAT CTGAACTTTG AG

22

2) INFORMATION FOR SEQ ID NO: 148

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148

AATGGCTTAT CAAAGTGAAT ATGC

24

2) INFORMATION FOR SEQ ID NO: 149

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149

TAATTCCTT TTTTCCATT CCTC

24

2) INFORMATION FOR SEQ ID NO: 150

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150

ACTAGAATCT CCAAATGAAT CCAGT

25

2) INFORMATION FOR SEQ ID NO: 151

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

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(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151

TGGAGTTAAT CTACGTCTCA TCTC

24

2) INFORMATION FOR SEQ ID NO: 152

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152

G TTCATACAG AAGACTCCTT TTTG

24

2) INFORMATION FOR SEQ ID NO: 153

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153

AGTTTTGATT ATCCGAATAA ATGCT

25

2) INFORMATION FOR SEQ ID NO: 154

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154

75/125

TTTAAATTCA GCTATATGGG GAGA

24

2) INFORMATION FOR SEQ ID NO: 155

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155

TTCCGTTTTG CTATTCCATA AT

22

2) INFORMATION FOR SEQ ID NO: 156

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156

CCTCTGATAA AAAACTTGTG AAAT

24

2) INFORMATION FOR SEQ ID NO: 157

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157

ACTACTCCTG GAATTACAAA CTGG

24

2) INFORMATION FOR SEQ ID NO: 158

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158

GCCAAAATTA AACCACAATC CAC

23

2) INFORMATION FOR SEQ ID NO: 159

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159

CATTTTGCTG AATGATAGTG CGTA

24

2) INFORMATION FOR SEQ ID NO: 160

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160

CGACCGGATT CCCACATCAA ATGATGCGGG TTGTGTTAAT TCCGGTCG

48

2) INFORMATION FOR SEQ ID NO: 161

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 bases
 - (B) TYPE: Nucleic acid

77/125

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161

CCCGCGCRTA GTTACTRCGT TGTAAGACGT CCGCGGG

37

2) INFORMATION FOR SEQ ID NO: 162

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162

CCCCGTAGTT ACTGCGTTGT AAGACGGGG

29

2) INFORMATION FOR SEQ ID NO: 163

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163

CCCGCGCATA GTTACTGCGT TGTAAGACGT CCGCGGG

37

2) INFORMATION FOR SEQ ID NO: 164

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164

CCCGCGCGTA GTTACTACGT TGTAAGACGT CCGCGGG

37

2) INFORMATION FOR SEQ ID NO: 165

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1282 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-9583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165

ACCATTTTAG	CTGTAGGGAA	ACTAAAAGAG	AAATATTGGA	AGCAAGCCAT	50
AGCAGAATAT	GAAAAACGTT	TAGGCCCAT	CACCAAGATA	GACATCATAG	100
AAGTTCCAGA	CGAAAAAGCA	CCAGAAAATA	TGAGCGACAA	AGAAATTGAG	150
CAAGTAAAAG	AAAAAGAAGG	CCAACGAATA	CTAGCCAAAA	TCAAACCACA	200
ATCCACAGTC	ATTACATTAG	AAATACAAGG	AAAGATGCTA	TCTTCCGAAG	250
GATTGGCCCA	AGAATTGAAC	CAACGCATGA	CCCAAGGGCA	AAGCGACTTT	300
GTATTCGTCA	TTGGCGGATC	AAACGGCCTG	CACAAGGACG	TCTTACAACG	350
CAGTAACTAT	GCACTATCAT	TTAGCAAAAT	GACATTCCCA	CATCAAATGA	400
TGCGGGTTGT	GTTAATTGAA	CAAGTGTATA	GAGCATTTAA	GATTATGCGT	450
GGAGAAGCGT	ACCACAAATA	AAACTAAAAA	ATATGAGAAA	ATTATTAAAT	500
TAGCTCAAAT	CTTTGAAGAA	TAAAAAGTGA	ATATTAAGTT	TGATAATTTA	550
GGTACAAGTA	AAGATTAAGA	ATTTCCATTA	TTTAATACAT	GGTGTGTAAA	600
TCGACTTCTT	TTTGTATTAG	ATGTTTGCAG	TAAGCGATGT	AAAGAAGATG	650
CTAATAAATA	TGTGAGGAAT	GATTACGATA	CTAGATAAGC	GGCTAATGAA	700
ATTTTTTAAA	GTACATATAT	AGACATATTT	TTCATTTAGT	AAAATTTTGA	750
ATTTCACTTT	GCTAAGACTA	GTGTCTAGAA	ATTTATAATG	ATTTATTAAC	800
ACCTATTTGA	AACTTAAGTA	TAATAAATGA	TTCGGATTTT	ATTTTTAATA	850
AAGACAAACT	TGAACGTAGC	AAAGTAGTTT	TTATGATAAA	TAATAAGTTT	900
TAATAATGTG	ACGCTTTTAT	ATAAGCACAT	TATTATGAAC	AATGTGAATT	950
GAGCATCTAC	AATTACATTA	ATAAATATAT	AAATGATGAT	TTAAATTCAC	1000
ATATATTTAT	AATACACATA	CTATATGAAA	GTTTTGATTA	TCCGAATAAA	1050
TGCTAAAATT	AATAAAATAA	TTAAAGGAAT	CATACTTATT	ATACGTATAC	1100
GTTTAGCTAC	TGAAC TACTG	GATTCATTTG	GAGATTCTAG	TAGTTCTTTT	1150
TCAATCTCTA	AATCTAAATC	AGTTTTGTAA	TAACCATTAA	TTCTTAATCT	1200
TTCATCTAGC	TCTGTACTTT	TTTCATCATT	TTTATCTTTG	TTGATATGTT	1250
CCATTTTCTC	GCCTCTTTTT	AATCAAGTAG	AA		1282

2) INFORMATION FOR SEQ ID NO: 166

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1108 bases
- (B) TYPE: Nucleic acid

79/125

- (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
(B) STRAIN: CCRI-9589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166

ACCATTTTAG	CTGTAGGGAA	ACTAAAAGAG	AAATATTGGA	AGCAAGCCAT	50
AGCAGAATAT	GAAAAACGTT	TAGGCCCATA	CACCAAGATA	GACATCATAG	100
AAGTTCCAGA	CGAAAAAGCA	CCAGAAAATA	TGAGCGACAA	AGAAATTGAG	150
CAAGTAAAAG	AAAAAGAAGG	CCAACGAATA	CTAGCCAAAA	TCAAACCACA	200
ATCCACAGTC	ATTACATTAG	AAATACAAGG	AAAGATGCTA	TCTTCCGAAG	250
GATTGGCCCA	AGAATTGAAC	CAACGCATGA	CCCAAGGGCA	AAGCGACTTT	300
GTATTTCGTCA	TTGGCGGATC	AAACGGCCTG	CACAAGGACG	TCTTACAACG	350
CAGTAACTAT	GCACTATCAT	TTAGCAAAAT	GACATTCCCA	CATCAAATGA	400
TGCGGGTTGT	GTTAATTGAA	CAAGTGTATA	GAGCATTTAA	GATTATGCGT	450
GGAGAAGCGT	ACCACAAATA	AAACTAAAAA	ATATGAGAAA	ATTATTAAAT	500
TAGCTCAAAT	CTTTGAAGAA	TAAAAAGTGA	ATATTAAGTT	TGATAATTTA	550
GGTACAAGTA	AAGATTAAAG	ATTTCCATTA	TTTAATACAT	GGTGTGTAAA	600
TCGACTTCTT	TTTGTATTAG	ATGTTTGCAG	TAAGCGATGT	AAAGAAGATG	650
CTAATAAATA	TGTGAGGAAT	GATTACGATA	CTAGATAAGC	GGCTAATGAA	700
ATTTTTTTAA	GTACATATAT	AGACATATTT	TTCATTTAGT	AAAATTTTGA	750
ATTTCACTTT	GCTAAGACTA	GTGTCTAGAA	ATTTATAATG	ATTTATTAAAC	800
ACCTATTTGA	AACTTAAGTA	TAATAAATGA	TTCGGATTTT	ATTTTTAATA	850
AAGACAAACT	TGAACGTAGC	AAAGTAGTTT	TTATGATAAA	TAATAAGTTT	900
TAATAATGTG	ACGCTTTTAT	ATAAGCACAT	TATTATGAAC	AATGTGAATT	950
GAGCATCTAC	AATTACATTA	ATAAATATAT	AAATGATGAT	TTAAATTCAC	1000
ATATATTTAT	AATACACATA	CTATATGAAA	GTTTGTGATTA	TCCGAATAAA	1050
TGCTAAAATT	AATAAAATAA	TTAAAGGAAT	CATACTTATT	ATACGTATAC	1100
GTTTAGCT					1108

2) INFORMATION FOR SEQ ID NO: 167

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1530 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
(B) STRAIN: CCRI-9860

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167

TTAGCTGTAG	GGAAACTAAA	AGAGAAATAT	TGGAAGCAAG	CCATAGCAGA	50
ATATGAAAAA	CGTTTAGGCC	CATACACCAA	GATAGACATC	ATAGAAGTTC	100

CAGACGAAAA	AGCACCAGAA	AATATGAGCG	ACAAAAGAAAT	TGAGCAAGTA	150
AAAGAAAAAG	AAGGCCAACG	AATACTAGCC	AAAATCAAAC	CACAATCCAC	200
AGTCATTACA	TTAGAAATAC	AAGGAAAGAT	GCTATCTTCC	GAAGGATTGG	250
CCCAAGAATT	GAACCAACGC	ATGACCCAAG	GGCAAAGCGA	CTTTGTATTCT	300
GTCATTGGCG	GATCAAACGG	CCTGCACAAG	GACGTCTTAC	AACGCAGTAA	350
CTATGCACTA	TCATTTAGCA	AAATGACATT	CCCACATCAA	ATGATGCGGG	400
TTGTGTTAAT	TGAACAAGTG	TATAGAGCAT	TTAAGATTAT	GCGTGGAGAA	450
GCATATCATA	AATGATGCGG	TTTTTTCAGC	CGCTTCATAA	AGGGGGGTGA	500
TCATATCGGA	ACGTATGAGG	TTTATGAGAA	TTGCTGCTAT	GTTTTTATGA	550
AGCGTATCAT	AAATGATGCA	GTTTTTGTATA	ATTTTTTCTT	TATCAGAGAT	600
TTTACTAAAA	ATCCCCTCAA	AGTTTGTTTT	TTTCAACTTC	AAC'TTTGAAG	650
GGAATAAATA	AGGAAC'TTAT	TTATATTTAT	CCTTTATCTC	ATTAATATCT	700
ATTTTTTTTAT	TAATAATATT	ATAAATATTA	AATTCTTTAG	AAAAGTCACT	750
ATCACTCTTA	TTCTTCATAC	TAAACGTTAT	TAATCTAATA	ATATCAGCTA	800
CTATTTCTTT	AAATTCTATT	GCATCTTCTT	TTTTATAAGT	AGCGCCTGTA	850
TGAACAATTT	TATTTCTCAT	ACCATAGTAA	TCTTTCATAT	ATTTTTTTTAC	900
ACAATTTTTTA	ATTTTCATTAG	AATTATCCAA	ATCTAGATTA	TCAATTGTCT	950
TTAATAAATG	ATCATTAACA	ACATTAGCAT	ACCCACATCC	AAGCTTCTTT	1000
TTTATCTCTT	CATCACTTAA	ATTTTCATCT	AATTTATAAT	ATCTTCTTAA	1050
AAAATTTGTG	ATAAAAACTT	CTAATGCAGT	CTGAATTTGT	ACAATTGCTA	1100
AATTATAGTC	AGATTTATAA	AAAGAACGTT	CACCTTTTCT	CATAGCCAAA	1150
ACATAAATAT	TGCTAGGATG	ATTATTGAAA	ATATTATAAT	TTTTTTTAAAT	1200
ATTTAATAAA	TCACTTTTTT	TGATAGATGA	ATACTGATCT	TCTTCTATCT	1250
TTCCAGGCAT	GTCAATCATG	AAAATACTCA	TCTCTTTTAT	ATTTCATCT	1300
ATAGTATATA	TTATATAATA	TGGAATACTT	AATATATCCC	CTAATGATAG	1350
CTGGTATATA	TTATGATACT	GATATTTAAC	GCTAATAATT	TTAATAAGAT	1400
TATTTAGACA	ATTAAATTGC	TTATTAAAAA	TTTTTCGTTAG	ACTATTACTT	1450
TTCTTTGATT	CCCTAGAAGT	AGAATTTGAT	TTCAATTTTT	TAAACTGATT	1500
GTGCTTGATT	ATTGAAGTTA	TTTCAACATA			1530

2) INFORMATION FOR SEQ ID NO: 168

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1256 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: CCRI-9681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168

GCTGTAGGGA	AACTAAAAGA	GAAATATTGG	AAGCAAGCCA	TAGCAGAATA	50
TGAAAAACGT	TTAGGCCCAT	ACACCAAGAT	AGACATCATA	GAAGTTCCAG	100
ACGAAAAAGC	ACCAGAAAAT	ATGAGCGACA	AAGAAATTGA	GCAAGTAAAA	150
GAAAAAGAAG	GCCAACGAAT	ACTAGCCAAA	ATTAAACCAC	AATCCACAGT	200
CATTACATTA	GAAATACAAG	GAAAGATGCT	ATCTTCCGAA	GGATTGGCCC	250
AAGAATTGAA	CCAACGCATG	ACCCAAGGGC	AAAGCGACTT	TGTATTTCGTC	300
ATTGGCGGAT	CAAACGGCCT	GCACAAGGAC	GTCTTACAAC	GCAGTAACTA	350
CGCACTATCA	TTCAAGCAAA	TGACATTCCC	ACATCAAATG	ATGCGGGTTG	400
TGTTAATTGA	GCAAGTGTAT	AGAGCATTTA	AGATTATGCG	TGGAGAAGCA	450

TATCATAAAT	GATGCGGTTT	TTTCAGCCGC	TTCATAAAGG	GATTTTGAAT	500
GTATCAGAAC	ATATGAGGTT	TATGTGAATT	GCTGTTATGT	TTTTAAGAAG	550
CATATCATAA	GTGATGCGGT	TTTTATTAAT	TAGTTGCTAA	AAAATGAAGT	600
ATGCAATATT	AATTATTATT	AAATTTTGAT	ATATTTAAAG	AAAGATTAAG	650
TTTAGGGTGA	ATGAATGGCT	TATCAAAGTG	AATATGCATT	AGAAAATGAA	700
GTA CTTCAAC	AACTTGAGGA	ATTGAACTAT	GAAAGAGTAA	ATATACATAA	750
TATTA AATTA	GAAATTAATG	AATATCTCAA	AGAACTAGGA	GTGTTGAAAA	800
ATGAATAAGC	AGACAAATAC	TCCAGAACTA	AGATTTCCAG	AGTTTGATGA	850
GGAATGGAAA	AAAAGGAAAT	TAGGTGAAGT	AGTAAATTAT	AAAAATGGTG	900
GTTCA TTTGA	AAGTTTAGTG	AAAAACCATG	GTGTATATAA	ACTCATAACT	950
CTTAAATCTG	TTAATACAGA	AGGAAAGTTG	TGTAATTCTG	GAAAATATAT	1000
CGATGATAAA	TGTGTTGAAA	CATTGTGTAA	TGATACTTTA	GTAATGATAC	1050
TGAGCGAGCA	AGCACCAGGA	CTAGTTGGAA	TGACTGCAAT	TATACCTAAT	1100
AATAATGAGT	ATGTACTAAA	TCAACGAGTA	GCAGCACTAG	TGCCTAAACA	1150
ATTTATAGAT	AGTCAATTTC	TATCTAAGTT	AATTAATAGA	AACCAGAAAT	1200
ATTTCA GTGT	GAGATCTGCT	GGAACAAAAG	TGAAAAATAT	TTCTAAAGGA	1250
CATGTA					1256

2) INFORMATION FOR SEQ ID NO: 169

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-9887

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169

TTACATTAGA	AATACAAGGA	AAGATGCTAT	CTTCCGAAGG	ATTGGCCCAA	50
GAATTGAACC	AACGCATGAC	CCAAGGGCAA	AGCGACTTTG	TTTTCGTCAT	100
TGGCGGATCA	AACGGCCTGC	ACAAGGACGT	CTTACAACGC	AGTAACTACG	150
CACTATCATT	CAGCAAAATG	ACATTCCCAC	ATCAAATGAT	GCGGGTTGTG	200
TTAATTGAAC	AAGTGTACAG	AGCATTTAAG	ATTATGCGAG	GAGAAGCTTA	250
TCATAAGTAA	TGAGGTTTCAT	GATTTTTGAC	ATAGTTAGCC	TCCGCAGTCT	300
TTCATTTCAA	GTAAATAATA	GCGAAATATT	CTTTATACTG	AATACTTATA	350
GTGAAGCAAA	GTTCTAGCTT	TGAGAAAATT	CTTTCTGCAA	CTAAATATAG	400
TAAATTACGG	TAAAATATAA	ATAAGTACAT	ATTGAAGAAA	ATGAGACATA	450
ATATATTTTA	TAATAGGAGG	GAATTTCAAA	TGATAGACAA	CTTTATGCAG	500
GTCCTTAAAT	TAATTTAAAGA	GAAACGTACC	AATAATGTAG	TTAAAAAATC	550
TGATTGGGAT	AAAGGTGATC	TATATAAAAC	TTTAGTCCAT	GATAAGTTAC	600
CCAAGCAGTT	AAAAGTGCAT	ATAAAAGAAG	ATAAATATTC	AGTTGTAGGG	650
AAGGTTGCTA	CTGGGAAC TA	TAGTAAAGTT	CCTTGGA TTT	CAATATATGA	700
TGAGAAATATA	ACAAAAGAAA	CAAAGGATGG	ATATTATTTG	GTATATCTTT	750
TTCATCCGGA	AGGAGAAGGC	ATATACTTAT	CTTTGAATCA	AGGATGGTCA	800
AAGATAAGTG	ATATGTTTCC	GCGGGATAAA	AATGCTGCAA	AACAAA	846

2) INFORMATION FOR SEQ ID NO: 170

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1270 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-9772

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170

CATTAGAAAT	ACAAGGAAAG	ATGCTATCTT	CCGAAGGATT	GGCCCAAGAA	50
TTGAACCAAC	GCATGACCCA	AGGGCAAAGC	GACTTTGTAT	TCGTCATTGG	100
CGGATCAAAC	GGCCTGCACA	AGGACGTCTT	ACAACGCAGT	AACTATGCAC	150
TATCAATTTAG	CAAAATGACA	TTCCCACATC	AAATGATGCG	GGTTGTGTTA	200
ATTGAACAAG	TGTATAGAGC	ATTTAAGATT	ATGCGTGGAG	AAGCATATCA	250
TAAATGATGC	GGTTTTTTCA	GCCGCTTCAT	AAAGGGATTT	TGAATGTATC	300
AGAACATATG	AGGTTTATGT	GAATTGCTGT	TATGTTTTTA	AGAAGCTTAT	350
CATAAGTAAT	GAGGTTTCATG	ATTTTTGACA	TAGTTAGCCT	CCGCAGTCTT	400
TCATTTCAAG	TAAATAATAG	CGAAATATTC	TTTATACTGA	ATACTTATAG	450
TGAAGCAAAG	TTCTAGCTTT	GAGAAAATTC	TTTCTGCAAC	TAAATATAGT	500
AAATTACGGT	AAAATATAAA	TAAGTACATA	TTGAAGAAAA	TGAGACATAA	550
TATATTTTAT	AATAGGAGGG	AATTTCAAAT	GATAGACAAC	TTTATGCAGG	600
TCCTTAAATT	AATTAAAGAG	AAACGTACCA	ATAATGTAGT	TAAAAAATCT	650
GATTGGGATA	AAGGTGATCT	ATATAAAACT	TTAGTCCATG	ATAAGTTACC	700
CAAGCAGTTA	AAAGTGCATA	TAAAAGAAGA	TAAATATTCA	GTTGTAGGGA	750
AGGTTGCTAC	TGGGAACTAT	AGTAAAGTTC	CTTGGATTTT	AATATATGAT	800
GAGAATATAA	CAAAAGAAAC	AAAGGATGGA	TATTATTTGG	TATATCTTTT	850
TCATCCGGAA	GGAGAAGGCA	TATACTTATC	TTTGAATCAA	GGATGGTCAA	900
AGATAAGTGA	TATGTTTCCG	CGGGATAAAA	ATGCTGCAAA	ACAAAGAGCA	950
TTAACTTTAT	CTTCCGAACT	CAATAAATAT	ATTACATCAA	ATGAATTTAA	1000
TACTGGAAGA	TTTTATTACG	CAGAAAATAA	AGATTCATCT	TATGATTTAA	1050
AAAATGATTA	TCCATCAGGA	TATTCTCATG	GATCAATAAG	ATTCAAATAT	1100
TATGATTTGA	ATGAAGGATT	CACAGAAGAA	GATATGCTAG	AGGATTTAAA	1150
GAAATTTTAA	GAACATTTTA	ATGAATTAGC	TTCAAAAAGT	ACAAAAACAT	1200
CCTATGATAG	CTTGGTCAAT	AGCATAGACG	AAATACAGGA	AGACAGCGAA	1250
ATTGAAGAAA	TTAGAACAGC				1270

2) INFORMATION FOR SEQ ID NO: 171

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 991 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: CCRI-9208

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171

ACCATTTTAG	CTGTAGGGAA	ACTAAAAGAG	AAATACTGGA	AGCAAGCCAT	50
AGCAGAATAT	GAAAAACGTT	TAGGCCCATATA	CACCAAGATA	GACATCATAG	100
AAGTTCAGAG	CGAAAAAGCA	CCAGAAAATA	TGAACTACAA	AGAAATTGAG	150
CAAGTAAAAG	AAAAAGAAGG	CCAACGAATA	CTAGCCAAAA	TCAAACCACA	200
ATCAACAGTC	ATTACATTAG	AAATACAAGG	AAAGATGCTA	TCTTCCGAAG	250
GATTGGCCCA	AGAATTGAAC	CAACGCATGA	CCCAAGGGCA	AAGCGACTTT	300
GTATTCGTCA	TTGGCGGATC	AAACGGCCTG	CACAAGGACG	TCTTACAACG	350
CAGTAACTAC	GCACTATCAT	TCAGCAAAAT	GACATTCCCA	CATCAAATGA	400
TGCGGGTTGT	GTTAATTGAA	CAAGTGTACA	GAGCATTTAA	GATTATGCGA	450
GGAGAAGCGT	ATCATAAGTG	ATGGTAAAAA	ATATGAGTAA	GTAGATGAAG	500
AGTGAAAATC	AGATTAATTA	ATAATAATGT	ATCAAATTTA	AATAAAGGGG	550
TTTTTTAAGTA	TGAATTTAAG	AGGTCATGAA	AATAGACTTA	AATTTTCATGC	600
GAAATATGAT	GTGACACCTA	TATCACATTT	AAAATTATTA	GAAGGTCAAA	650
AGAAAGACGG	TGAAGGCGGC	ATACTGACAG	ATAGCTATTA	CTGTTTTTCA	700
TACAGCTTAA	AAGGTAATTC	TAAAAAAGTT	TTAGGTACGT	TTAATTGTGG	750
TTATCATATT	GCTGAAGATT	TACTAAAATT	ATCAAATCAA	GATAAATTAC	800
CTTTATTTAA	CCCGTTTAAA	GTAATTAATG	AAGGTAATCA	ATTGCAGGGC	850
GTAACGAATA	AAGGTAATTT	AAATATTAAT	AGGCAAGAA	AACAGTATAA	900
TGAAGTGGCT	TTACAGCTTT	CAAATGCTAT	TAATTTAATC	ATAATTTGTT	950
ATGAGGATAA	TATTAAAGAA	CCACTTTCAA	CGATAAAATA	C	991

2) INFORMATION FOR SEQ ID NO: 172

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 748 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: CCRI-9770

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172

ATCGTTTAAC	GTGTCACATG	ATGCGATAGA	TCCGCAATTT	TATATTTTCC	50
ATAATAACTA	TAAGAAGTTT	ACGATTTTAA	CAGATACGGG	TTACGTGTCT	100
GATCGTATGA	AAGGTATGAT	ACGTGGCAGC	GATGCATTTA	TTTTTGAGAG	150
TAATCATGAC	GTCGATATGT	TGAGAATGTG	TCGTTATCCA	TGGAAGACGA	200
AACAACGCAT	TTTAGGCGAT	ATGGGTCATG	TATCTAATGA	GGATGCGGGT	250
CATGCGATGA	CAGACGTGAT	TACAGGTAAC	ACGAAACGTA	TTTACTTATC	300
GCATTTTATCA	CAAGATAATA	ATATGAAAGA	TTTGGCGCGT	ATGAGTGTG	350
GCCAAGTATT	GAACGAACAC	GATATTGATA	CGGAAAAAGA	AGTATTGCTA	400
TGTGATACGG	ATAAAGCTAT	TCCAACACCA	ATATATACAA	TATAAATGAG	450
AGTCATCCGA	TAAAGTTCCG	CACTGCTGTG	AAACGACTTT	ATCGGGTGCT	500
TTTTTATGTT	GTTGGTGGGA	AATGGCTGTT	GTTGAGTTGA	ATCGGATTGA	550
TTGAAATGTG	TAAATAAATT	CGATATTAAA	TGTAATTTAT	AAATAATTTA	600

CATAAAATCA	AACATTTTAA	TATAAGGATT	ATGATAATAT	ATTGGTGTAT	650
GACAGTTAAT	GGAGGGAACG	AAATGAAAGC	TTTATTACTT	AAAACAAGTG	700
TATGGCTCGT	TTTGCTTTTT	AGTGTGATGG	GATTATGGCA	TGTCTCGA	748

2) INFORMATION FOR SEQ ID NO: 173

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 917 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-9864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173

AAATACAAGG	AAAGATGCTA	TCTTCCGAAG	GATTGGCCCA	AGAATTGAAC	50
CAACGCATGA	CCCAAGGGCA	AAGCGACTTT	GTATTCGTCA	TTGGCGGATC	100
AAACGGCCTG	CACAAGGACG	TCTTACAACG	TAGTAACTAC	GCACTATCAT	150
TCAGCAAAAT	GACATTCCCA	CATCAAATGA	TGCGGGTTGT	GTTAATTGAG	200
CAAGTGTATA	GAGCATTTAA	GATTATGCGT	GGAGAAGCAT	ATCATAAATG	250
ATGCGGTTTT	TTCAGCCGCT	TCATAAAGGG	ATTTTGAATG	TATCAGAACA	300
TATGAGGTTT	ATGTGAATTG	CTGTTATGTT	TTTAAGAAGC	TTATCATAAG	350
TAATGAGGTT	CATGATTTTT	GACATAGTTA	GCCTCCGCAG	TCTTTCATTT	400
CAAGTAAATA	ATAGCGAAAT	ATTCTTTTATA	CTGAATACTT	ATAGTGAAGC	450
AAAGTTCTAG	CTTTGAGAAA	ATTCTTTTCTG	CAACTAAATA	TAGTAAATTA	500
CGGTAAATA	TAAATAAGTA	CATATTGAAG	AAAATGAGAC	ATAATATATT	550
TTATAATAGG	AGGGAATTTC	AAATGATAGA	CAACTTTATG	CAGGTCCTTA	600
AATTAATTAA	AGAGAAACGT	ACCAATAATG	TAGTTAAAAA	ATCTGATTGG	650
GATAAAGGTG	ATCTATATAA	AACTTTAGTC	CATGATAAGT	TACCCAAGCA	700
GTTAAAAGTG	CATATAAAAG	AAGATAAATA	TTCAGTTGTA	GGGAAGGTTG	750
CTACTGGGAA	CTATAGTAAA	GTTCCTTGGA	TTTCAATATA	TGATGAGAAT	800
ATAACAAAAG	AAACAAAGGA	TGGATATTAT	TTGGTATATC	TTTTTCATCC	850
GGAAGGAGAA	GGCATATACT	TATCTTTGAA	TCAAGGATGG	TCAAAGATAA	900
GTGATATGTT	TCCGCGG				917

2) INFORMATION FOR SEQ ID NO: 174

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1132 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: CCRI-9865

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174

GCTGTAGGGA	AACTAAAAGA	GAAATATTGG	AAGCAAGCCA	TAGCAGAATA	50
TGAAAAACGT	TTAGGCCCAT	ACACCAAGAT	AGACATCATA	GAAGTTCCAG	100
ACGAAAAAGC	ACCAGAAAAT	ATGAGCGACA	AAGAAATTGA	GCAAGTAAAA	150
GAAAAAGAAG	GCCAACGAAT	ACTAGCCAAA	ATCAAACCAC	AATCAACAGT	200
CATTACATTA	GAAATACAAG	GAAAGATGCT	ATCTTCCGAA	GGATTGGCCC	250
AAGAATTGAA	CCAACGCATG	ACCCAAGGGC	AAAGCGACTT	TGTATTTCGTC	300
ATTGGCGGAT	CAAACGGCCT	GCACAAGGAC	GTCTTACAAC	GTAGTAACTA	350
CGCACTATCA	TTCAGCAAAA	TGACATTCCC	ACATCAAATG	ATGCGGGTTG	400
TGTTAATTGA	GCAAGTGTAT	AGAGCATTTA	AGATTATGCG	TGGAGAAGCA	450
TATCATAAAT	GATGCGGTTT	TTTCAGCCGC	TTCATAAAGG	GATTTTGAAT	500
GTATCAGAAC	ATATGAGGTT	TATGTGAATT	GCTGTTATGT	TTTTAAGAAG	550
CTTATCATAA	GTAATGAGGT	TCATGATTTT	TGACATAGTT	AGCCTCCGCA	600
GTCTTTTCATT	TCAAGTAAAT	AATAGCGAAA	TATTCTTTAT	ACTGAATACT	650
TATAGTGAAG	CAAAGTTCTA	GCTTTGAGAA	AATTCTTTCT	GCAACTAAAT	700
ATAGTAAATT	ACGGTAAAAAT	ATAAATAAGT	ACATATTGAA	GAAAATGAGA	750
CATAATATAT	TTTATAATAG	GAGGGAATTT	CAAATGATAG	ACAACTTTAT	800
GCAGGTCCTT	AAATTAATTA	AAGAGAAACG	TACCAATAAT	GTAGTTAAAA	850
AATCTGATTG	GGATAAAGGT	GATCTATATA	AAACTTTAGT	CCATGATAAG	900
TTACCCAAGC	AGTTAAAAGT	GCATATAAAA	GAAGATAAAT	ATTCAGTTGT	950
AGGGAAGGTT	GCTACTGGGA	ACTATAGTAA	AGTTCCTTGG	ATTTCAATAT	1000
ATGATGAGAA	TATAACAAAA	GAAACAAAGG	ATGGATATTA	TTTGGTATAT	1050
CTTTTTTCATC	CGGAAGGAGA	AGGCATATAC	TTATCTTTGA	ATCAAGGATG	1100
GTCAAAGATA	AGTGATATGT	TTCCGCGGGA	TA		1132

2) INFORMATION FOR SEQ ID NO: 175

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1133 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Staphylococcus aureus
(B) STRAIN: CCRI-9866

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175

AGCTGTAGGG	AAACTAAAAG	AGAAATATTG	GAAGCAAGCC	ATAGCAGAAT	50
ATGAAAAACG	TTTAGGCCCA	TACACCAAGA	TAGACATCAT	AGAAGTTCCA	100
GACGAAAAAG	CACCAGAAAA	TATGAGCGAC	AAAGAAATTG	AGCAAGTAAA	150
AGAAAAAGAA	GGCCAACGAA	TACTAGCCAA	AATCAAACCA	CAATCAACAG	200
TCATTACATT	AGAAATACAA	GGAAAGATGC	TATCTTCCGA	AGGATTGGCC	250
CAAGAATTGA	ACCAACGCAT	GACCCAAGGG	CAAAGCGACT	TTGTATTTCGT	300
CATTGGCGGA	TCAAACGGCC	TGCACAAGGA	CGTCTTACAA	CGTAGTAACT	350
ACGCACTATC	ATTCAGCAAA	ATGACATTCC	CACATCAAAT	GATGCGGGTT	400
GTGTTAATTG	AGCAAGTGTA	TAGAGCATTT	AAGATTATGC	GTGGAGAAGC	450

ATATCATAAA	TGATGCGGTT	TTTTTCAGCCG	CTTCATAAAG	GGATTTTGGAA	500
TGTATCAGAA	CATATGAGGT	TTATGTGAAT	TGCTGTTATG	TTTTTAAGAA	550
GCTTATCATA	AGTAATGAGG	TTCATGATTT	TTGACATAGT	TAGCCTCCGC	600
AGTCTTTCAT	TTCAAGTAAA	TAATAGCGAA	ATATTCTTTA	TACTGAATAC	650
TTATAGTGAA	GCAAAGTTCT	AGCTTTGAGA	AAATTCTTTC	TGCAACTAAA	700
TATAGTAAAT	TACGGTAAAA	TATAAATAAG	TACATATTGA	AGAAAATGAG	750
ACATAATATA	TTTTATAATA	GGAGGGAATT	TCAAATGATA	GACAACTTTA	800
TGCAGGTCCT	TAAATTAATT	AAAGAGAAAC	GTACCAATAA	TGTAGTTAAA	850
AAATCTGATT	GGGATAAAGG	TGATCTATAT	AAAACTTTAG	TCCATGATAA	900
GTTACCCAAG	CAGTTAAAAG	TGCATATAAA	AGAAGATAAA	TATTCAGTTG	950
TAGGGAAGGT	TGCTACTGGG	AACTATAGTA	AAGTTCCTTG	GATTTCAATA	1000
TATGATGAGA	ATATAACAAA	AGAAACAAAG	GATGGATATT	ATTTGGTATA	1050
TCTTTTTCAT	CCGGAAGGAG	AAGGCATATA	CTTATCTTTG	AATCAAGGAT	1100
GGTCAAAGAT	AAGTGATATG	TTTCCGCGGG	ATA		1133

2) INFORMATION FOR SEQ ID NO: 176

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1087 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: CCRI-9867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176

ACTAAAAGAG	AAATATTGGA	AGCAAGCCAT	AGCAGAATAT	GAAAAACGTT	50
TAGGCCCAT	CACCAAGATA	GACATCATAG	AAGTTCAGCA	CGAAAAAGCA	100
CCAGAAAATA	TGAGCGACAA	AGAAATTGAG	CAAGTAAAAG	AAAAAGAAGG	150
CCAACGAATA	CTAGCCAAAA	TCAAACCACA	ATCAACAGTC	ATTACATTAG	200
AAATACAAGG	AAAGATGCTA	TCTTCCGAAG	GATTGGCACA	AGAATTGAAC	250
CAACGCATGA	CCCAAGGGCA	AAGCGACTTT	GTATTCTGTC	TTGGCGGATC	300
AAACGGCCTG	CACAAGGACG	TCTTACAACG	TAGTAACTAC	GCACTATCAT	350
TCAGCAAAAT	GACATTCCCA	CATCAAATGA	TGCGGGTTGT	GTTAATTGAG	400
CAAGTGTATA	GAGCGTTTAA	GATTATGCGT	GGAGAAGCAT	ATCATAAATG	450
ATGCGGTTTT	TTCAGCCGCT	TCATAAAGGG	ATTTTGAATG	TATCAGAACA	500
TATGAGGTTT	ATGTGAATTG	CTGTTATGTT	TTTAAGAAGC	TTATCATAAG	550
TAATGAGGTT	CATGATTTTT	GACATAGTTA	GCCTCCGCAG	TCTTTCATTT	600
CAAGTAAATA	ATAGCGAAAT	ATTCTTTTATA	CTGAATACTT	ATAGTGAAGC	650
AAAGTTCTAG	CTTTGAGAAA	ATTCTTTCTG	CAACTAAATA	TAGTAAATTA	700
CGGTAAAATA	TAAATAAGTA	CATATTGAAG	AAAATGAGAC	ATAATATATT	750
TTATAATAGG	AGGGAATTTC	AAATGATAGA	CAACTTTATG	CAGGTCCTTA	800
AATTAATTAA	AGAGAAACGT	ACCAATAATG	TAGTTAAAAA	ATCTGATTGG	850
GATAAAGGTG	ATCTATATAA	AACTTTAGTC	CATGATAAGT	TACCCAAGCA	900
GTTAAAAGTG	CATATAAAAG	AAGATAAATA	TTCAGTTGTA	GGGAAGGTTG	950
CTACTGGGAA	CTATAGTAAA	GTTCCCTTGA	TTTCAATATA	TGATGAGAAT	1000
ATAACAAAAG	AAACAAAGGA	TGGATATTAT	TTGGTATATC	TTTTTTCATCC	1050
GGAAGGAGAA	GGCATATACT	TATCTTTGAA	TCAAGGA		1087

2) INFORMATION FOR SEQ ID NO: 177

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 903 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-9868

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177

CAAGGAAAGA	TGCTATCTTC	CGAAGGATTG	GCCCAAGAAT	TGAACCAACG	50
CATGACCCAA	GGGCAAAGCG	ACTTTGTATT	CGTCATTGGC	GGATCAAACG	100
GCCTGCACAA	GGACGTCTTA	CAACGTAGTA	ACTACGCACT	ATCATTCAGC	150
AAAATGACAT	TCCCACATCA	AATGATGCGG	GTTGTGTAA	TTGAGCAAGT	200
GTATAGAGCA	TTTAAGATTA	TGCGTGGAGA	AGCATATCAT	AAATGATGCG	250
GTTTTTTCAG	CCGCTTCATA	AAGGGATTTT	GAATGTATCA	GAACATATGA	300
GGTTTATGTG	AATTGCTGTT	ATGTTTTTAA	GAAGCTTATC	ATAAGTAATG	350
AGGTTTCATGA	TTTTTGACAT	AGTTAGCCTC	CGCAGTCTTT	CATTTCAAGT	400
AAATAATAGC	GAAATATTCT	TTTACTGAA	TACTTATAGT	GAAGCAAAGT	450
TCTAGCTTTG	AGAAAATTCT	TTCTGCAACT	AAATATAGTA	AATTACGGTA	500
AAATATAAAT	AAGTACATAT	TGAAGAAAAT	GAGACATAAT	ATATTTTATA	550
ATAGGAGGGA	ATTTCAAATG	ATAGACAACT	TTATGCAGGT	CCTTAAATTA	600
ATTAAAGAGA	AACGTACCAA	TAATGTAGTT	AAAAAATCTG	ATTGGGATAA	650
AGGTGATCTA	TATAAAACTT	TAGTCCATGA	TAAGTTACCC	AAGCAGTTAA	700
AAGTGCATAT	AAAAGAAGAT	AAATATTCAG	TTGTAGGGAA	GGTTGCTACT	750
GGGAACTATA	GTAAAGTTCC	TTGGATTTC	ATATATGATG	AGAATATAAC	800
AAAAGAAACA	AAGGATGGAT	ATTATTTGGT	ATATCTTTT	CATCCGGAAG	850
GAGAAGGCAT	ATACTTATCT	TTGAATCAAG	GATGGTCAAA	GATAAGTGAT	900
ATG					903

2) INFORMATION FOR SEQ ID NO: 178

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1114 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-9869

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178

GGAAACTAAA	AGAGAAATAT	TGGAAGCAAG	CCATAGCAGA	ATATGAAAAA	50
CGTTTAGGCC	CATACACCAA	GATAGACATC	ATAGAAGTTC	CAGACGAAAA	100
AGCACCAGAA	AATATGAGCG	ACAAAGAAAT	TGAGCAAGTA	AAAGAAAAAG	150
AAGGCCAACG	AATACTAGCC	AAAATCAAAC	CACAATCAAC	AGTCATTACA	200
TTAGAAATAC	AAGGAAAGAT	GCTATCTTCC	GAAGGATTGG	CCCAAGAATT	250
GAACCAACGC	ATGACCCAAG	GGCAAAGCGA	CTTTGTATTTC	GTCATTGGCG	300
GATCAAACGG	CCTGCACAAG	GACGTCTTAC	AACGTAAGTAA	CTACGCACTA	350
TCATTTCAGCA	AAATGACATT	CCCACATCAA	ATGATGCGGG	TTGTGTTAAT	400
TGAGCAAGTG	TATAGAGCAT	TTAAGATTAT	GCGTGGAGAA	GCATATCATA	450
AATGATGCGG	TTTTTTTCAGC	CGCTTCATAA	AGGGATTTTG	AATGTATCAG	500
AACATATGAG	GTTTATGTGA	ATTGCTGTTA	TGTTTTTAAG	AAGCTTATCA	550
TAAGTAATGA	GGTTCATGAT	TTTTTGACATA	GTTAGCCTCC	GCAGTCTTTC	600
ATTTCAAGTA	AATAATAGCG	AAATATTCTT	TATACTGAAT	ACTTATAGTG	650
AAGCAAAGTT	CTAGCTTTGA	GAAAATTCTT	TCTGCAACTA	AATATAGTAA	700
ATTACGGTAA	AATATAAATA	AGTACATATT	GAAGAAAATG	AGACATAATA	750
TATTTTATAA	TAGGAGGGAA	TTTCAAATGA	TAGACAACCTT	TATGCAGGTC	800
CTTAAATTAA	TTAAAGAGAA	ACGTACCAAT	AATGTAGTTA	AAAAATCTGA	850
TTGGGATAAA	GGTGATCTAT	ATAAACTTTT	AGTCCATGAT	AAGTTACCCA	900
AGCAGTTAAA	AGTGCATATA	AAAGAAGATA	AATATTCAGT	TGTAGGGAAG	950
GTTGCTACTG	GGAAGTATAG	TAAAGTTCCT	TGGATTTCAA	TATATGATGA	1000
GAATATAACA	AAAGAAACAA	AGGATGGATA	TTATTTGGTA	TATCTTTTTC	1050
ATCCGGAAGG	AGAAGGCATA	TACTTATCTT	TGAATCAAGG	ATGGTCAAAG	1100
ATAAGTGATA	TGTT				1114

2) INFORMATION FOR SEQ ID NO: 179

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1121 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: CCRI-9871

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179

GGAAACTAAA	AGAGAAATAT	TGGAAGCAAG	CCATAGCAGA	ATATGAAAAA	50
CGTTTAGGCC	CATACACCAA	GATAGACATC	ATAGAAGTTC	CAGACGAAAA	100
AGCACCAGAA	AATATGAGCG	ACAAAGAAAT	TGAGCAAGTA	AAAGAAAAAG	150
AAGGCCAACG	AATACTAGCC	AAAATCAAAC	CACAATCCAC	AGTCATTACA	200
TTAGAAATAC	AAGGAAAGAT	GCTATCTTCC	GAAGGATTGG	CCCAAGAATT	250
GAACCAACGC	ATGACCCAAG	GGCAAAGCGA	CTTTGTATTTC	GTCATTGGCG	300
GATCAAACGG	CCTGCACAAG	GACGTCTTAC	AACGCAAGTAA	CTATGCACTA	350
TCATTTAGCA	AAATGACATT	CCCACATCAA	ATGATGCGGG	TTGTGTTAAT	400
TGAACAAGTG	TATAGAGCAT	TTAAGATTAT	GCGTGGAGAA	GCATATCATA	450
AATGATGCGG	TTTTTTTCAGC	CGCTTCATAA	AGGGATTTTG	AATGTATCAG	500
AACATATGAG	GTTTATGTGA	ATTGCTGTTA	TGTTTTTAAG	AAGCTTATCA	550
TAAGTAATGA	GGTTCATGAT	TTTTTGACATA	GTTAGCCTCC	GCAGTCTTTC	600
ATTTCAAGTA	AATAATAGCG	AAATATTCTT	TATACTGAAT	ACTTATAGTG	650
AAGCAAAGTT	CTAGCTTTGA	GAAAATTCTT	TCTGCAACTA	AATATAGTAA	700

ATTACGGTAA	AATATAAATA	AGTACATATT	GAAGAAAATG	AGACATAATA	750
TATTTTATAA	TAGGAGGGAA	TTTCAAATGA	TAGACAACTT	TATGCAGGTC	800
CTTAAATTAA	TTAAAGAGAA	ACGTACCAAT	AATGTAGTTA	AAAAATCTGA	850
TTGGGATAAA	GGTGATCTAT	ATAAAACTTT	AGTCCATGAT	AAGTTACCCA	900
AGCAGTTAAA	AGTGCATATA	AAAGAAGATA	AATATTCAGT	TGTAGGGAAG	950
GTTGCTACTG	GGAACATAG	TAAAGTTCCT	TGGATTTCAA	TATATGATGA	1000
GAATATAACA	AAAGAAACAA	AGGATGGATA	TTATTTGGTA	TATCTTTTTC	1050
ATCCGGAAGG	AGAAGGCATA	TACTTATCTT	TGAATCAAGG	ATGGTCAAAG	1100
ATAAGTGATA	TGTTTCCGCG	G			1121

2) INFORMATION FOR SEQ ID NO: 180

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1121 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: CCRI-9872

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180

TAGCTGTAGG	GAAACTAAAA	GAGAAATATT	GGAAGCAAGC	CATAGCAGAA	50
TATGAAAAAC	GTTTAGGCC	ATACACCAAG	ATAGACATCA	TAGAAAGTTCC	100
AGACGAAAAA	GCACCAGAAA	ATATGAGCGA	CAAAGAAATT	GAGCAAGTAA	150
AAGAAAAAGA	AGGCCAACGA	ATACTAGCCA	AAATCAAACC	ACAATCCACA	200
GTCATTACAT	TAGAAATACA	AGGAAAGATG	CTATCTTCCG	AAGGATTGGC	250
CCAAGAATTG	AACCAACGCA	TGACCCAAGG	GCAAAGCGAC	TTTGTATTTCG	300
TCATTGGCGG	ATCAAACGGC	CTGCACAAGG	ACGTCTTACA	ACGCAGTAAC	350
TATGCACTAT	CATTTAGCAA	AATGACATTC	CCACATCAAA	TGATGCGGGT	400
TGTGTTAATT	GAACAAGTGT	ATAGAGCATT	TAAGATTATG	CGTGGAGAAG	450
CATATCATAA	ATGATGCGGT	TTTTTCAGCC	GCTTCATAAA	GGGATTTTGA	500
ATGTATCAGA	ACATATGAGG	TTTATGTGAA	TTGCTGTTAT	GTTTTTAAGA	550
AGCTTATCAT	AAGTAATGAG	GTTCATGATT	TTTGACATAG	TTAGCCTCCG	600
CAGTCTTTCA	TTTCAAGTAA	ATAATAGCGA	AATATTCTTT	ATACTGAATA	650
CTTATAGTGA	AGCAAAGTTC	TAGCTTTGAG	AAAATTCTTT	CTGCAACTAA	700
ATATAGTAAA	TTACGGTAAA	ATATAAATAA	GTACATATTG	AAGAAAATGA	750
GACATAATAT	ATTTTATAAT	AGGAGGGAAT	TTCAAATGAT	AGACAACTTT	800
ATGCAGGTCC	TTAAATTAAT	TAAAGAGAAA	CGTACCAATA	ATGTAGTTAA	850
AAAATCTGAT	TGGGATAAAG	GTGATCTATA	TAAAACCTTA	GTCCATGATA	900
AGTTACCCAA	GCAGTTAAAA	GTGCATATAA	AAGAAGATAA	ATATTCAGTT	950
GTAGGGAAGG	TTGCTACTGG	GAAGTATAGT	AAAGTTCCTT	GGATTTCAAT	1000
ATATGATGAG	AATATAACAA	AAGAAACAAA	GGATGGATAT	TATTTGGTAT	1050
ATCTTTTTTCA	TCCGGAAGGA	GAAGGCATAT	ACTTATCTTT	GAATCAAGGA	1100
TGGTCAAAGA	TAAGTGATAT	G			1121

2) INFORMATION FOR SEQ ID NO: 181

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1131 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-9873

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181

CTGTAGGGAA	ACTAAAAGAG	AAATATTGGA	AGCAAGCCAT	AGCAGAATAT	50
GAAAAACGTT	TAGGCCCAT	CACCAAGATA	GACATCATAG	AAGTTCCAGA	100
CGAAAAAGCA	CCAGAAAATA	TGAGCGACAA	AGAAATTGAG	CAAGTAAAAG	150
AAAAAGAAGG	CCAACGAATA	CTAGCCAAAA	TCAAACCACA	ATCCACAGTC	200
ATTACATTAG	AAATACAAGG	AAAGATGCTA	TCTTCCGAAG	GATTGGCCCA	250
AGAATTGAAC	CAACGCATGA	CCCAAGGGCA	AAGCGACTTT	GTATTCGTCA	300
TTGGCGGATC	AAACGGCCTG	CACAAGGACG	TCTTACAACG	CAGTAACTAT	350
GCACTATCAT	TTAGCAAAAT	GACATTCCCA	CATCAAATGA	TGCGGGTTGT	400
GTTAATTGAA	CAAGTGTATA	GAGCATTTAA	GATTATGCGT	GGAGAAGCAT	450
ATCATAAATG	ATGCGGTTTT	TTCAGCCGCT	TCATAAAGGG	ATTTTGAATG	500
TATCAGAACA	TATGAGGTTT	ATGTGAATTG	CTGTTATGTT	TTTAAGAAGC	550
TTATCATAAG	TAATGAGGTT	CATGATTTTT	GACATAGTTA	GCCTCCGCAG	600
TCTTTCATTT	CAAGTAAATA	ATAGCGAAAT	ATTCTTTATA	CTGAATACTT	650
ATAGTGAAGC	AAAGTTCTAG	CTTTGAGAAA	ATTCTTTCTG	CAACTAAATA	700
TAGTAAATTA	CGGTAAAATA	TAAATAAGTA	CATATTGAAG	AAAATGAGAC	750
ATAATATATT	TTATAATAGG	AGGGAATTTT	AAATGATAGA	CAACTTTATG	800
CAGGTCCTTA	AATTAATTAA	AGAGAAACGT	ACCAATAATG	TAGTTAAAAA	850
ATCTGATTGG	GATAAAGGTG	ATCTATATAA	AACTTTAGTC	CATGATAAGT	900
TACCCAAGCA	GTTAAAAGTG	CATATAAAAAG	AAGATAAATA	TTCAGTTGTA	950
GGGAAGGTTG	CTACTGGGAA	CTATAGTAAA	GTTCCCTTGA	TTTCAATATA	1000
TGATGAGAAT	ATAACAAAAG	AAACAAAGGA	TGGATATTAT	TTGGTATATC	1050
TTTTTTCATCC	GGAAGGAGAA	GGCATATACT	TATCTTTGAA	TCAAGGATGG	1100
TCAAAGATAA	GTGATATGTT	TCCGCGGGAT	A		1131

2) INFORMATION FOR SEQ ID NO: 182

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 896 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-9874

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182

CATTAGAAAT	ACAAGGAAAG	ATGCTATCTT	CCGAAGGATT	GGCCCAAGAA	50
TTGAACCAAC	GCATGACCCA	AGGGCAAAGC	GACTTTGTAT	TCGTCATTGG	100
CGGATCAAAC	GGCCTGCACA	AGGACGTCTT	ACAACGCAGT	AACTATGCAC	150
TATCATTTTAG	CAAAATGACA	TTCCACATC	AAATGATGCG	GGTTGTGTTA	200
ATTGAACAAG	TGTATAGAGC	ATTTAAGATT	ATGCGTGGAG	AAGCATATCA	250
TAAATGATGC	GGTTTTTTCA	CCCGCTTCAT	AAAGGGATTT	TGAATGTATC	300
AGAACATATG	AGGTTTATGT	GAATTGCTGT	TATGTTTTTA	AGAAGCTTAT	350
CATAAGTAAT	GAGGTTTCATG	ATTTTTGACA	TAGTTAGCCT	CCGCAGTCTT	400
TCATTTCAAG	TAAATAATAG	CGAAATATTC	TTTATACTGA	ATACTTATAG	450
TGAAGCAAAG	TTCTAGCTTT	GAGAAAATTC	TTTCTGCAAC	TAAATATAGT	500
AAATTACGGT	AAAATATAAA	TAAGTACATA	TTGAAGAAAA	TGAGACATAA	550
TATATTTTAT	AATAGGAGGG	AATTTCAAAT	GATAGACAAC	TTTATGCAGG	600
TCCTTAAATT	AATTAAAGAG	AAACGTACCA	ATAATGTAGT	TAAAAAATCT	650
GATTGGGATA	AAGGTGATCT	ATATAAAACT	TTAGTCCATG	ATAAGTTACC	700
CAAGCAGTTA	AAAGTGCATA	TAAAAAGAAG	TAAATATTTCA	GTTGTAGGGA	750
AGGTTGCTAC	TGGGAACTAT	AGTAAAGTTC	CTTGGATTTT	AATATATGAT	800
GAGAATATAA	CAAAAGAAAC	AAAGGATGGA	TATTATTTGG	TATATCTTTT	850
TCATCCGGAA	GGAGAAGGCA	TATACTTATC	TTTGAATCAA	GGATGG	896

2) INFORMATION FOR SEQ ID NO: 183

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1125 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: CCRI-9875

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183

GGAAACTAAA	AGAGAAATAT	TGGAAGCAAG	CCATATCAGA	ATATGAAAAA	50
CGTTTAGGCC	CATACACCAA	GATAGACATC	ATAGAAGTTC	CAGACGAAAA	100
AGCACCAGAA	AATATGAGCG	ACAAAGAAAT	CGAGCAAGTA	AAAGAAAAAG	150
AAGGCCAACG	AATACTAGCC	AAAATCAAAC	CACAATCAAC	AGTCATTACA	200
TTAGAAATAC	AAGGAAAGAT	GCTATCTTCC	GAAGGATTGG	CTCAAGAATT	250
GAACCAACGC	ATGACCCAAG	GGCAAAGCGA	CTTTGTATTTC	GTTATTGGCG	300
GATCAAACGG	CCTGCACAAG	GACGTCTTAC	AACGCAGTAA	CTATGCACCTA	350
TCATTTCAGCA	AAATGACATT	TCCACATCAG	ATGATGCGGG	TTGTGTTAAT	400
TGAGCAAGTG	TATAGAGCAT	TAAAGATTAT	GCGTGGGGAA	GCATATCATA	450
AATGATGCGG	TTTTTTTCAGC	CGCTTCATAA	AGGGATTTTG	AATGTATCAG	500
AACATATGAG	GTTTATGTGA	ATTGCTGTGA	TGTTTTTAAG	AAGCTTATCA	550
TAAGTAATGA	GGTTCATGAT	TTTTTGACATA	GTTAGCCTCC	GCAGTCTTTC	600
ATTTCAAGTA	AATAATAGCG	AAATATTCTT	TATACTGAAT	ACTTATAGTG	650
AAGCAAAGTT	CTAGCTTTGA	GAAAATTCTT	TCTGCAACTA	AATATAGTAA	700
ATTACGGTAA	AATATAAATA	AGTACATATT	GAAGAAAAATG	AGACATAATA	750
TATTTTATAA	TAGGAGGGAA	TTTCAAATGA	TAGACAACCTT	TATGCAGGTC	800
CTTAAATTAA	TTAAAGAGAA	ACGTACCAAT	AATGTAGTTA	AAAAATCTGA	850
TTGGGATAAA	GGTGATCTAT	ATAAACTTTT	AGTCCATGAT	AAGTTACCCA	900
AGCAGTTAAA	AGTGCATATA	AAAGAAGATA	AATATTCACT	TGTAGGGAAG	950

GTTGCTACTG	GGAAGTATAG	TAAAGTTCCT	TGGATTTCAT	TATATGATGA	1000
GAATATAACA	AAAGAAACAA	AGGATGGATA	TTATTGGGTA	TATCTTTTTC	1050
ATCCGGAAGG	AGAAGGCATA	TACTTATCTT	TGAATCAAGG	ATGGTCAAAG	1100
ATAAGTGATA	TGTTTCCGCG	GGATA			1125

2) INFORMATION FOR SEQ ID NO: 184

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 679 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-9876

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184

ATAAGAGGGA	ACAGTGTGAA	CAAGTTAATA	ACTTGTGGAT	AACTGGAAAG	50
TTGATAACAA	TTTGGAGGAC	CAAACGACAT	GAAAATCACC	ATTTTAGCTG	100
TAGGGAAACT	AAAAGAGAAA	TATTGGAAGC	AAGCCATAGC	AGAATATGAA	150
AAACGTTTAG	GCCCATACAC	CAAGATAGAC	ATCATAGAAG	TTCCAGACGA	200
AAAAGCACCA	GAAAATATGA	GCGACAAAGA	AATTGAGCAA	GTAAAAGAAA	250
AAGAAGGCCA	ACGAATACTA	GCCAAAATCA	AACCACAATC	CACAGTCATT	300
ACATTAGAAA	TACAAGGAAA	GATGCTATCT	TCCGAAGGAT	TGGCCCAAGA	350
ATTGAACCAA	CGCATGACCC	AAGGGCAAAG	CGACTTTGTA	TTCGTCATTG	400
GCGGATCAAA	CGGCCTGCAC	AAGGACGTCT	TACAACGCAG	TAACATATGCA	450
CTATCATTTA	GCAAAATGAC	ATTCCCACAT	CAAATGATGC	GGGTTGTGTT	500
AATTGAACAA	GTGTATAGAG	CATTTAAGAT	TATGCGTGGA	GAGGCTTATC	550
ATAAATAAAA	CTAAAAATTA	GATTGTGTAT	AATTTAAAAA	TTTAATGAGA	600
TGTGGAGGAA	TTACATATAT	GAAATATTGG	AGTATACCTT	GCAATATCAT	650
ACGATGTTTA	TAGAGTGTTT	AATAAACCA			679

2) INFORMATION FOR SEQ ID NO: 185

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1125 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-9882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185

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GGAAACTAAA	AGAGAAATAT	TGGAAGCAAG	CCATAGCAGA	ATATGAAAAA	50
CGTTTAGGCC	CATACACCAA	GATAGACATC	ATAGAAGTTC	CAGACGAAAA	100
AGCACCAGAA	AATATGAGCG	ACAAAGAAAT	TGAGCAAGTA	AAAGAAAAAG	150
AAGGCCAACG	AATACTAGCC	AAAATCAAAC	CACAATCAAC	AGTCATTACA	200
TTAGAAATAC	AAGGAAAGAT	GCTATCTTCC	GAAGGATTGG	CACAAGAATT	250
GAACCAACGC	ATGACCCAAG	GGCAAAGCGA	CTTTGTATTG	GTCATTGGCG	300
GATCAAACGG	CCTGCACAAG	GACGTCTTAC	AACGTAGTAA	CTACGCACTA	350
TCATTTCAGCA	AAATGACATT	CCCACATCAA	ATGATGCGGG	TTGTGTTAAT	400
TGAGCAAGTG	TATAGAGCGT	TTAAGATTAT	GCGTGGAGAA	GCATATCATA	450
AATGATGCGG	TTTTTTTCAGC	CGCTTCATAA	AGGGATTTTG	AATGTATCAG	500
AACATATGAG	GTTTATGTGA	ATTGCTGTTA	TGTTTTTAAG	AAGCTTATCA	550
TAAGTAATGA	GGTTCATGAT	TTTTGACATA	GTTAGCCTCC	GCAGTCTTTC	600
ATTTCAAGTA	AATAATAGCG	AAATATTCTT	TATACTGAAT	ACTTATAGTG	650
AAGCAAAGTT	CTAGCTTTGA	GAAAATTCTT	TCTGCAACTA	AATATAGTAA	700
ATTACGGTAA	AATATAAATA	AGTACATATT	GAAGAAAATG	AGACATAATA	750
TATTTTATAA	TAGGAGGGAA	TTTCAAATGA	TAGACAACTT	TATGCAGGTC	800
CTTAAATTAA	TTAAAGAGAA	ACGTACCAAT	AATGTAGTTA	AAAAATCTGA	850
TTGGGATAAA	GGTGATCTAT	ATAAACTTTT	AGTCCATGAT	AAGTTACCCA	900
AGCAGTTAAA	AGTGCATATA	AAAGAAGATA	AATATTCAGT	TGTAGGGAAG	950
GTTGCTACTG	GGAACATAG	TAAAGTTCCT	TGGATTTCAG	TATATGATGA	1000
GAATATAACA	AAAGAAACAA	AGGATGGATA	TTATTTGGTA	TATCTTTTTC	1050
ATCCGGAAGG	AGAAGGCATA	TACTTATCTT	TGAATCAAGG	ATGGTCAAAG	1100
ATAAGTGATA	TGTTTCCGCG	GGATA			1125

2) INFORMATION FOR SEQ ID NO: 186

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 926 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: CCRI-9885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186

TACATTAGAA	ATACAAGGAA	AGATGCTATC	TTCCGAAGGA	TTGGCCCAAG	50
AATTGAACCA	ACGCATGACC	CAAGGGCAAA	GCGACTTTGT	ATTTCGTCATT	100
GGCGGATCAA	ACGGCCTGCA	CAAGGACGTC	TTACAACGCA	GTAACATATGC	150
ACTATCATTT	AGCAAAATGA	CATTCCCACA	TCAAATGATG	CGGGTTGTGT	200
TAATTGAACA	AGTGTATAGA	GCATTTAAGA	TTATGCGTGG	AGAAGCATAT	250
CATAAATGAT	GCGGTTTTTT	CAGCCGCTTC	ATAAAGGGAT	TTTGAATGTA	300
TCAGAACATA	TGAGGTTTAT	GTGAATTGCT	GTTATGTTTT	TAAGAAGCTT	350
ATCATAAGTA	ATGAGGTTCA	TGATTTTTGA	CATAGTTAGC	CTCCGCAGTC	400
TTTCATTTCA	AGTAAATAAT	AGCGAAATAT	TCTTTTACT	GAATACTTAT	450
AGTGAAGCAA	AGTTCCTAGCT	TTGAGAAAAT	TCTTTCTGCA	ACTAAATATA	500
GTAAATTACG	GTAAAATATA	AATAAGTACA	TATTGAAGAA	AATGAGACAT	550
AATATATTTT	ATAATAGGAG	GGAATTTCAA	ATGATAGACA	ACTTTATGCA	600
GGTCCTTAAA	TTAATTAAAG	AGAAACGTAC	CAATAATGTA	GTTAAAAAAT	650
CTGATTGGGA	TAAAGGTGAT	CTATATAAAA	CTTTAGTCCA	TGATAAGTTA	700

CCCAAGCAGT	TAAAAGTGCA	TATAAAAGAA	GATAAATATT	CAGTTGTAGG	750
GAAGGTTGCT	ACTGGGAACT	ATAGTAAAGT	TCCTTGGAAT	TCAATATATG	800
ATGAGAATAT	AACAAAAGAA	ACAAAGGATG	GATATTATTT	GGTATATCTT	850
TTTCATCCGG	AAGGAGAAGG	CATATACTTA	TCTTTGAATC	AAGGATGGTC	900
AAAGATAAGT	GATATGTTTC	CGCGGG			926

2) INFORMATION FOR SEQ ID NO: 187

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187

GGATGTGGGT ATGCTAATGT TGTT

24

2) INFORMATION FOR SEQ ID NO: 188

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188

TGAACAATTT TATTTCTCAT ACCATAG

27

2) INFORMATION FOR SEQ ID NO: 189

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2154 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-9583

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189

CGGTAATAAA	AAATACGATA	TAGATGAATA	ACAAAACAGT	GAAGCAATCC	50
GTAACGATGG	TTGCTTCACT	GTTTTATTAT	GAATTATTAA	TAAGTGCTGT	100
TACTTCTCCC	TTAAATACAA	TTTCTTCATT	TTCATTGTAT	GTTGAAAGTG	150
ACACTGTAAC	GAGTCCATTT	TCTTTTTTTA	TGGATTTCTT	ATTTGTAATT	200
TCAGCGATAA	CGTACAATGT	ATTACCTGGG	TATACAGGTT	TAATAAATTT	250
AACGTTATTC	ATTTGTGTTC	CTGCTACAAC	TTCTTCTCCG	TATTTACCTT	300
CTTCTACCCA	TAATTTAAAT	GATATTGAAA	GTGTATGCAT	GCCAGATGCA	350
ATGATACCTT	TAAATCTACT	TTGTTCTGCT	TTTTCCTTAT	CTATATGCAT	400
ATATTGAGGA	TCAAAAGTTG	TTGCAAATTG	GATAATTCT	TCTTCTGTAA	450
TATGAAGGCT	TTTTGTTTTG	AATGTTTCTC	CTACTATAAA	ATCATCGTAT	500
TTCATATATG	TCTCTCTTTC	TTATTCAAAT	TAATTTTTTA	GTATGTAACA	550
TGTTAAAGGT	AAGTCTACCG	TCACTGAAAC	GTAAGACTCA	CCTCTAACTT	600
TCTATTGAGA	CAAATGCACC	ATTTTATCTG	CATTGTCTGT	AAAGATACCA	650
TCAACTCCCC	AATTAGCAAG	TTGGTTTGCA	CGTGCTGGTT	TGTTTACAGT	700
CCATACGTTT	AATTCATAAC	CCGCTTCTTT	TACCATTTTT	ACTTTTGCTT	750
TAGTAAGTTT	GGCATCTTCA	GTGTTTACTA	TTTTAGCATT	ACAGTAATCT	800
AAAAGTGTTT	TCCAGTCTTC	ACGAAACGAA	GTTGTATGGA	ATATAACTGC	850
TCTGTTATAT	TGTGGCATGA	TTTCTTCTGC	AAGTTTAACA	AGCACAACAT	900
TAAAGCTTGA	AATGAGCACT	TCTTGATTCT	GATTTAAGTT	TGTTAATTGT	950
TCTTCCACTT	GCTTAACCAT	ACTTTTAGAA	AGTGCTAGTC	CATTCGGTCC	1000
AGTAATACCT	TTTAATTCTA	CATTTAAATT	CATATTATAT	TCATTTGCTA	1050
TTTTTACTAC	ATCATCGAAA	GTTGGCAAAT	GTTTCATCTT	GAATTTTTCA	1100
CCAAACCAAG	ATCCTGCAGA	AGCATCTTTA	ATTTTCATCAT	AATTC AATTC	1150
AGTTATTTCC	CCGGACATAT	TTGTAGTCCG	TTCTAAATAA	TCATCATGAA	1200
TGATAATCAG	TTGTTCACTT	TTTGTAATTG	CAACATCTAA	CTCCAACCAG	1250
TTTATACCTT	CTACTTCTGA	AGCAGCTTTA	AATGATGCAA	TTGTATTTTC	1300
CGGAGCTTTA	CTAGGTAATC	CTCTATGTCC	ATATACAGTT	AGCATATTAC	1350
CTCTCCTTGC	ATTTTTTATTT	TTTTAATTAA	CGTAACTGTA	TTATCACATT	1400
AATCGCACTT	TTATTTCCAT	TAAAAAGAGA	TGAATATCAT	AAATAAAGAA	1450
GTCGATAGAT	TCGTATTGAT	TATGGAGTTA	ATCTACGTCT	CATCTCATT	1500
TTAAAAAATC	ATTTATGTCC	CAAGCTCCAT	TTTGTAATCA	AGTCTAGTTT	1550
TTCGGTTCTG	TTGCAAAGTT	GAATTTATAG	TATAATTTTA	ACAAAAAGGA	1600
GTCTTCTGTA	TGAAC TATTT	CAGATATAAA	CAATTTAACA	AGGATGTTAT	1650
CACTGTAGCC	GTTGGCTACT	ATCTAAGATA	TACATTGAGT	TATCGTGATA	1700
TATCTGAAAT	ATTAAGGGAA	CGTGGTGTA	ACGTTCAATCA	TTCAACGGTC	1750
TACCGTTGGG	TTCAAGAATA	TGCCCAATT	TTGTATCAAA	TTTGGAAGAA	1800
AAAGCATAAA	AAAGCTTATT	ACAAATGGCG	TATTGATGAG	ACGTACATCA	1850
AAATAAAAGG	AAAATGGAGC	TATTTATATC	GTGCCATTGA	TGCAGAGGGA	1900
CATACATTAG	ATATTTGGTT	GCGTAAGCAA	CGAGATAATC	ATTCAGCATA	1950
TGCGTTTATC	AAACGTCTCA	TTAAACAATT	TGGTAAACCT	CAAAAGGTAA	2000
TTACAGATAT	GGCACCTTCA	ACGAAGGTAG	CAATGGCTAA	AGTAATTAAA	2050
GCTTTTAAAC	TTAAACCTGA	CTGTCATTGT	ACATCGAAAT	ATCTGAATAA	2100
CCTCATTGAG	CAAGATCACC	GTCATATTAA	AGTAAGAAAG	ACAAGGTATC	2150
AAAG					2154

2) INFORMATION FOR SEQ ID NO: 190

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2410 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

(B) STRAIN: CCRI-9504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190

CCACCTTCAT	ATGACGTCTA	TCCATTTATG	TATGGCATGA	GTAACGAAGA	50
ATATAATAAA	TTAACCGAAG	ATAAAAAAGA	ACCTCTGCTC	AACAAGTTCC	100
AGATTACAAC	TTCACCAGGT	TCAACTCAAA	AAATATTAAC	AGCAATGATT	150
GGGTTAAATA	ACAAAACATT	AGACGATAAA	ACAAGTTATA	AAATCGATGG	200
TAAAGGTTGG	CAAAAAGATA	AATCTTGGGG	TGGTTACAAC	GTTACAAGAT	250
ATGAAGTGGT	AAATGGTAAT	ATCGACTTAA	AACAAGCAAT	AGAATCATCA	300
GATAACATTT	TCTTTGCTAG	AGTAGCACTC	GAATTAGGCA	GTAAGAAATT	350
TGAAAAAGGC	ATGAAAAAAC	TAGGTGTTGG	TGAAGATATA	CCAAGTGATT	400
ATCCATTTTA	TAATGCTCAA	ATTTCAAACA	AAAATTTAGA	TAATGAAATA	450
TTATTAGCTG	ATTCAGGTTA	CGGACAAGGT	GAAATACTGA	TTAACCCAGT	500
ACAGATCCTT	TCAATCTATA	GCGCATTAGA	AAATAATGGC	AATATTAACG	550
CACCTCACTT	ATTAAAAGAC	ACGAAAAACA	AAGTTTGGAA	GAAAAATATT	600
ATTTCCAAAG	AAAATATCAA	TCTATTAACT	GATGGTATGC	AACAAGTCGT	650
AAATAAAACA	CATAAAGAAG	ATATTATAG	ATCTTATGCA	AACTTAATTG	700
GCAAATCCGG	TACTGCAGAA	CTCAAAATGA	AACAAGGAGA	AACTGGCAGA	750
CAAATTGGGT	GGTTTATATC	ATATGATAAA	GATAATCCAA	ACATGATGAT	800
GGCTATTAA	GTTAAAGATG	TACAAGATAA	AGGAATGGCT	AGCTACAATG	850
CCAAAATCTC	AGGTAAAGTG	TATGATGAGC	TATATGAGAA	CGGTAATAAA	900
AAATACGATA	TAGATGAATA	ACAAAACAGT	GAAGCAATCC	GTAACGATGG	950
TTGCTTCACT	GTTTTATTAT	GAATTATTAA	TAAGTGCTGT	TACTTCTCCC	1000
TTAAATACAA	TTTCTTCATT	TTCATTGTAT	GTTGAAAGTG	AACTGTAAAC	1050
GAGTCCATTT	TCTTTTTTTA	TGGATTCTCT	ATTTGTAATT	TCAGCGATAA	1100
CGTACAATGT	ATTACCTGGG	TATACAGGTT	TAATAAATTT	AACGTTATTC	1150
ATTTGTGTTT	CTGCTACAAC	TTCTTCTCCG	TATTTACCTT	CTTCTACCCA	1200
TAATTTAAAT	GATATTGAAA	GTGTATGCAT	GCCAGATGCA	ATGATACCTT	1250
TAAATCTACT	TTGTTCTGCT	TTTTCTTTAT	CTATATGCAT	ATATTGAGGA	1300
TCAAAAGTTG	TTGCAAATTG	GATAATTTCT	TCTTCTGTAA	TATGAAGGCT	1350
TTTTGTTTTG	AATGTTTCTC	CTACTATAAA	ATCATCGTAT	TTCATATATG	1400
TCTCTCTTTT	TTATTCAAAT	TAATTTTTTA	GTATGTAACA	TGTTAAAGGT	1450
AAGTCTACCG	TCACTGAAAC	GTAAGACTCA	CCTCTAACTT	TCTATTGAGA	1500
CAAATGCACC	ATTTTATCTG	CATTGTCTGT	AAAGATACCA	TCAACTCCCC	1550
AATTAGCAAG	TTGGTTTGCA	CGTGCTGGTT	TGTTTACAGT	CCATACGTTT	1600
AATTCATAAC	CCGCTTCTTT	TACCATTTTT	ACTTTTGCTT	TAGTAAGTTT	1650
GGCATCTTCA	GTGTTTACTA	TTTTAGCATT	ACAGTAATCT	AAAAGTGTTT	1700
TCCAGTCTTC	ACGAAACGAA	GTTGTATGGA	ATATAACTGC	TCTGTTATAT	1750
TGTGGCATGA	TTTCTTCTGC	AAGTTTAACA	AGCACAACAT	TAAAGCTTGA	1800
AATGAGCACT	TCTTGATTCT	GATTTAAGTT	TGTTAATTGT	TCTTCCACTT	1850
GCTTAACCAT	ACTTTTAGAA	AGTGCTAGTC	CATTGGGTCC	AGTAATACCT	1900
TTTAATTCTA	CATTTAAATT	CATATTATAT	TCATTTGCTA	TTTTTACTAC	1950
ATCATCGAAA	GTTGGCAAAT	GTTTCATCTT	GAATTTTTCA	CCAAACCAAG	2000
ATCCTGCAGA	AGCATCTTTA	ATTTTCATCAT	AATTCAATTC	AGTTATTTCC	2050
CCGGACATAT	TTGTAGTCCG	TTCTAAATAA	TCATCATGAA	TGATAATCAG	2100
TTGTTTCATCT	TTTGTAATTG	CAACATCTAA	CTCCAACCAG	TTTATACCTT	2150
CTACTTCTGA	AGCAGCTTTA	AATGATGCAA	TTGTATTTTC	CGGAGCTTTA	2200
CTAGGTAATC	CTCTATGTCC	ATATAACAGT	AGCATATTAC	CTCTCCTTGC	2250
ATTTTTTATTT	TTTTAATTAA	CGTAACTGTA	TTATCACATT	AATCGCACTT	2300
TTATTTCCAT	TAAAAAGAGA	TGAATATCAT	AAATAAAGAA	GTCGATAGAT	2350
TCGTATTGAT	TATGGAGTTA	ATCTACGTCT	CATCTCATTT	TTAAAAAATC	2400
ATTTATGTCC					2410

2) INFORMATION FOR SEQ ID NO: 191

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1858 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: CCRI-9208

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191

CACCTTCATA	TGACGTCTAT	CCATTTATGT	ATGGCATGAG	TAACGAAGAA	50
TATAATAAAT	TAACCGAAGA	TAAAAAAGAA	CCTCTGCTCA	ACAAGTTCCA	100
GATTACAAC	TCACCAGGTT	CAACTCAAAA	AATATTAACA	GCAATGATTG	150
GGTTAAATAA	CAAAACATTA	GACGATAAAA	CAAGTTATAA	AATCGATGGT	200
AAAGGTTGGC	AAAAAGATAA	ATCTTGGGGT	GGTTACAACG	TTACAAGATA	250
TGAAGTGGTA	AATGGTAATA	TCGACTTAAA	ACAAGCAATA	GAATCATCAG	300
ATAACATTTT	CTTTGCTAGA	GTAGCACTCG	AATTAGGCAG	TAAGAAATTT	350
GAAAAAGGCA	TGAAAAAACT	AGGTGTTGGT	GAAGATATAC	CAAGTGATTA	400
TCCATTTTAT	AATGCTCAAA	TTTCAAACAA	AAATTTAGAT	AATGAAATAT	450
TATTAGCTGA	TTCAGGTTAC	GGACAAGGTG	AAATACTGAT	TAACCCAGTA	500
CAGATCCTTT	CAATCTATAG	CGCATTAGAA	AATAATGGCA	ATATTAACGC	550
ACCTCACTTA	TTAAAAGACA	CGAAAAACAA	AGTTTGAAG	AAAAATATTA	600
TTTCCAAAGA	AAATATCAAT	CTATTAAC	ATGGTATGCA	ACAAGTCGTA	650
AATAAAACAC	ATAAAGAAGA	TATTTATAGA	TCTTATGCAA	ACTTAATTGG	700
CAAATCCGGT	ACTGCAGAAC	TCAAAATGAA	ACAAGGAGAA	ACTGGCAGAC	750
AAATTGGGTG	GTTTATATCA	TATGATAAAG	ATAATCCAAA	CATGATGATG	800
GCTATTAATG	TTAAAGATGT	ACAAGATAAA	GGAATGGCTA	GCTACAATGC	850
CAAAATCTCA	GGTAAAGTGT	ATGATGAGCT	ATATGAGAAC	GGTAATAAAA	900
AATACGATAT	AGATGAATAA	CAAAACAGTG	AAGCAATCCG	TAACGATGGT	950
TGCTTCACTG	TTTTATTATG	AATTATTAAT	AAGTGCTGTT	ACTTCTCCCT	1000
TAAATACAAT	TTCTTCATTT	GCATTGTATG	TTGAAAGTGA	CACGTGAACG	1050
AGTCCATTTT	CTTTTTTTTAT	TGATTTCTTA	TTTGTAATTT	CAGCGATAAC	1100
GTACAATGTA	TTACCTGGGT	ATACAGGTTT	AATAAATTTA	ACGTTATTCA	1150
TTTGTGTTCC	TGCTACAACT	TCTTCTCCGT	ATTTACCTTC	TTCTACCCAT	1200
AATTTAAATG	ATATTGAAAG	TGTATGCATG	CCAGATGCAA	TGATACCTTT	1250
AAATCTACTT	TGTTCTGCTT	TTTCTTTATC	TATATGCATA	TATTGAGGAT	1300
CAAAAGTTGT	TGCAAATTGG	ATAATTTCTT	CTTCTGTAAT	ATGAAGGCTT	1350
TTTGTTTTGA	ATGTTTCTCC	TACTATAAAA	TCATCGTATT	TCATATATGT	1400
CTCTCTTTCT	TATTCAAATT	AATTTTTTTAG	TATGTAACAT	GTTAAAGGTA	1450
AGTCTACCGT	CACTGAAACG	TAAGACTCAC	CTCTAACTTT	CTATTGAGAC	1500
AAATGCACCA	TTTTATCTGC	ATTGTCTGTA	AAGATAACCAT	CAACTCCCCA	1550
ATTAGCAAGT	TGGTTTGCAC	GTGCTGGTTT	GTTTACAGTC	CATACGTTCA	1600
ATTCATAACC	CGCTTCTTTT	ACCATTTTTA	CTTTTGCTTT	AGTAAGTTTG	1650
GCATCTTCAG	TGTTTACTAT	TTTAGCATT	CAGTAATCTA	AAAGTGTTCT	1700
CCAGTCTTCA	CGAAACGAAG	TTGTATGGAA	TATAACTGCT	CTGTTATATT	1750
GTGGCATGAT	TTCTTCTGCA	AGTTTAACAA	GCACAACATT	AAAGCTTGAA	1800
ATGAGCACTT	CTTGATTCTG	ATTTAAGTTT	GTTAATTGTT	CTTCCACTTG	1850
CTTAACCA					1858

2) INFORMATION FOR SEQ ID NO: 192

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1861 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: CCRI-9589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192

CCACCTTCAT	ATGACGTCTA	TCCATTTATG	TATGGCATGA	GTAACGAAGA	50
ATATAATAAA	TTAACCGAAG	ATAAAAAAGA	ACCTCTGCTC	AACAAGTTCC	100
AGATTACAAC	TTCACCAGGT	TCAACTCAA	AAATATTAAC	AGCAATGATT	150
GGGTAAATA	ACAAAACATT	AGACGATAAA	ACAAGTTATA	AAATCGATGG	200
TAAAGGTTGG	CAAAAAGATA	AATCTTGGGG	TGGTTACAAC	GTTACAAGAT	250
ATGAAGTGGT	AAATGGTAAT	ATCGACTTAA	AACAAGCAAT	AGAATCATCA	300
GATAACATTT	TCTTTGCTAG	AGTAGCACTC	GAATTAGGCA	GTAAGAAATT	350
TGAAAAAGGC	ATGAAAAAAC	TAGGTGTTGG	TGAAGATATA	CCAAGTGATT	400
ATCCATTTTA	TAATGCTCAA	ATTTCAAACA	AAAATTTAGA	TAATGAAATA	450
TTATTAGCTG	ATTCAGGTTA	CGGACAAGGT	GAAATACTGA	TTAACCCAGT	500
ACAGATCCTT	TCAATCTATA	GCGCATTAGA	AAATAATGGC	AATATTAACG	550
CACCTCACTT	ATTAAAAGAC	ACGAAAAACA	AAGTTTGGAA	GAAAAATATT	600
ATTTCCAAAG	AAAATATCAA	TCTATTAACT	GATGGTATGC	AACAAGTCGT	650
AAATAAAACA	CATAAAGAAG	ATATTTATAG	ATCTTATGCA	AACTTAATTG	700
GCAAAATCCGG	TACTGCAGAA	CTCAAATGA	AACAAGGAGA	AACTGGCAGA	750
CAAATTGGGT	GGTTTATATC	ATATGATAAA	GATAATCCAA	ACATGATGAT	800
GGCTATTAAT	GTTAAAGATG	TACAAGATAA	AGGAATGGCT	AGCTACAATG	850
CCAAAATCTC	AGGTAAAGTG	TATGATGAGC	TATATGAGAA	CGGTAATAAA	900
AAATACGATA	TAGATGAATA	ACAAAACAGT	GAAGCAATCC	GTAACGATGG	950
TTGCTTCACT	GTTTTATTAT	GAATTATTAA	TAAGTGCTGT	TACTTCTCCC	1000
TTAAATACAA	TTTCTTCATT	TTCATTGTAT	GTTGAAAGTG	AACTGTAAAC	1050
GAGTCCATTT	TCTTTTTTTA	TGGATTTCTT	ATTTGTAATT	TCAGCGATAA	1100
CGTACAATGT	ATTACCTGGG	TATACAGGTT	TAATAAATTT	AACGTTATTC	1150
ATTTGTGTTT	CTGCTACAAC	TTCTTCTCCG	TATTTACCTT	CTTCTACCCA	1200
TAATTTAAAT	GATATTGAAA	GTGTATGCAT	GCCAGATGCA	ATGATACCTT	1250
TAAATCTACT	TTGTTCTGCT	TTTTCTTTAT	CTATATGCAT	ATATTGAGGA	1300
TCAAAAGTTG	TTGCAAATTG	GATAATTTCT	TCTTCTGTAA	TATGAAGGCT	1350
TTTTGTTTTG	AATGTTTCTC	CTACTATAAA	ATCATCGTAT	TTCATATATG	1400
TCTCTCTTTC	TTATTCAAAT	TAATTTTTTA	GTATGTAACA	TGTTAAAGGT	1450
AAGTCTACCG	TCACTGAAAC	GTAAGACTCA	CCTCTAACTT	TCTATTGAGA	1500
CAAATGCACC	ATTTTATCTG	CATTGCTCTG	AAAGATACCA	TCAACTCCCC	1550
AAATTAGCAAG	TTGGTTTGCA	CGTGCTGGTT	TGTTTACAGT	CCATACGTTT	1600
AATTCATAAC	CCGCTTCTTT	TACCATTTTT	ACTTTTGCTT	TAGTAAGTTT	1650
GGCATCTTCA	GTGTTTACTA	TTTTAGCATT	ACAGTAATCT	AAAAGTGTTT	1700
TCCAGTCTTC	ACGAAACGAA	GTTGTATGGA	ATATAACTGC	TCTGTTATAT	1750
TGTGGCATGA	TTTCTTCTGC	AAGTTTAAAC	AGCACACAT	TAAAGCTTGA	1800
AATGAGCACT	TCTTGATTCT	GATTAAAGTT	TGTTAATTGT	TCTTCCACTT	1850
GCTTAACCAT	A				1861

2) INFORMATION FOR SEQ ID NO: 193

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1861 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: CCRI-9681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193

CCACCTTCAT	ATGACGTCTA	TCCATTTATG	TATGGCATGA	GTAACGAAGA	50
ATATAATAAA	TTAACCGAAG	ATAAAAAAGA	ACCTCTGCTC	AACAAGTTCC	100
AGATTACAAC	TTCACCAGGT	TCAACTCAAA	AAATATTAAC	AGCAATGATT	150
GGGTAAATA	ACAAAACATT	AGACGATAAA	ACAAGTTATA	AAATCGATGG	200
TAAAGGTTGG	CAAAAAGATA	AATCTTGGGG	TGGTTACAAC	GTTACAAGAT	250
ATGAAGTGGT	AAATGGTAAT	ATCGACTTAA	AACAAGCAAT	AGAATCATCA	300
GATAACATTT	TCTTTGCTAG	AGTAGCACTC	GAATTAGGCA	GTAAGAAATT	350
TGAAAAAGGC	ATGAAAAAAC	TAGGTGTTGG	TGAAGATATA	CCAAGTGATT	400
ATCCATTTTA	TAATGCTCAA	ATTTCAAACA	AAAATTTAGA	TAATGAAATA	450
TTATTAGCTG	ATTCAGGTTA	CGGACAAGGT	GAAATACTGA	TTAACCCAGT	500
ACAGATCCTT	TCAATCTATA	GCGCATTAGA	AAATAATGGC	AATATTAACG	550
CACCTCACTT	ATTAAAAGAC	ACGAAAAACA	AAGTTTGGAA	GAAAAATATT	600
ATTTCCAAAG	AAAATATCAA	TCTATTAACT	GATGGTATGC	AACAAGTCGT	650
AAATAAAACA	CATAAAGAAG	ATATTTATAG	ATCTTATGCA	AACTTAATTG	700
GCAAATCCGG	TACTGCAGAA	CTCAAAATGA	AACAAGGAGA	AACTGGCAGA	750
CAAATTGGGT	GGTTTATATC	ATATGATAAA	GATAATCCAA	ACATGATGAT	800
GGCTATTAAT	GTTAAAGATG	TACAAGATAA	AGGAATGGCT	AGCTACAATG	850
CCAAAATCTC	AGGTAAAGTG	TATGATGAGC	TATATGAGAA	CGGTAATAAA	900
AAATACGATA	TAGATGAATA	ACAAAACAGT	GAAGCAATCC	GTAACGATGG	950
TTGCTTCACT	TTTTTATTAT	GAATTATTAA	TAAAGTGCTGT	TACTTCTCCC	1000
TTAAATACAA	TTTCTTCATT	TTCATTGTAT	GTTGAAAGTG	ACACTGTAAC	1050
GAGTCCATTT	TCTTTTTTTA	TGGATTCTTT	ATTTGTAATT	TCAGCGATAA	1100
CGTACAATGT	ATTACCTGGG	TATACAGGTT	TAATAAATTT	AACGTTATTC	1150
ATTTGTGTTT	CTGCTACAAC	TTCTTCTCCG	TATTTACCTT	CTTCTACCCA	1200
TAATTTAAAT	GATATTGAAA	GTGTATGCAT	GCCAGATGCA	ATGATACCTT	1250
TAAATCTACT	TTGTTCTGCT	TTTTCTTTAT	CTATATGCAT	ATATTGAGGA	1300
TCAAAAGTTG	TTGCAAATTG	GATAATTTCT	TCTTCTGTAA	TATGAAGGCT	1350
TTTTGTTTTG	AATGTTTCTC	CTACTATAAA	ATCATCGTAT	TTCATATATG	1400
TCTCTCTTTC	TTATTCAAAT	TAATTTTTTTA	GTATGTAACA	TGTTAAAGGT	1450
AAGTCTACCG	TCACTGAAAC	GTAAGACTCA	CCTCTAACTT	TCTATTGAGA	1500
CAAATGCACC	ATTTTATCTG	CATTGTCTGT	AAAGATACCA	TCAACTCCCC	1550
AATTAGCAAG	TTGGTTTGCA	CGTGCTGGTT	TGTTTACAGT	CCATACGTTT	1600
AATTCATAAC	CCGCTTCTTT	TACCATTTTT	ACTTTTGCTT	TAGTAAGTTT	1650
GGCATCTTCA	GTGTTTACTA	TTTTAGCATT	ACAGTAATCT	AAAAGTGTTT	1700
TCCAGTCTTC	ACGAAACGAA	GTTGTATGGA	ATATAACTGC	TCTGTTATAT	1750
TGTGGCATGA	TTTCTTCTGC	AAGTTTAACA	AGCACAACAT	TAAAGCTTGA	1800
AATGAGCACT	TCTTGATTCT	GATTTAAGTT	TGTTAATTGT	TCTTCCACTT	1850
GCTTAACCAT	A				1861

2) INFORMATION FOR SEQ ID NO: 194

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1052 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: CCRI-9772

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194

CGGTAATAAA	AAATACGATA	TAGATGAATA	ACAAAACAGT	GAAGCAATCC	50
GTAACGATGG	TTGCTTCACT	GTTTTATTAT	GAATTATTAA	TAAGTGCTGT	100
TACTTCTCCC	TTAAATACAA	TTTCTTCATT	TTCATTGTAT	GTTGAAAGTG	150
ACACTGTAAC	GAGTCCATTT	TCTTTTTTTA	TGGATTTCTT	ATTTGTAATT	200
TCAGCGATAA	CGTACAATGT	ATTACCTGGG	TATACAGGTT	TAATAAATTT	250
AACGTTATTC	ATTTGTGTTC	CTGCTACAAC	TTCTTCTCCG	TATTTACCTT	300
CTTCTACCCA	TAATTTAAAT	GATATTGAAA	GTGTATGCAT	GCCAGATGCA	350
ATGATACCTT	TAAATCTACT	TTGTTCTGCT	TTTTCTTTAT	CTATATGCAT	400
ATATTGAGGA	TCAAAAGTTG	TTGCAAATTG	GATAATTTCT	TCTTCTGTAA	450
TATGAAGGCT	TTTTGTTTTG	AATGTTTCTC	CTACTATAAA	ATCATCGTAT	500
TTCATATATG	TCTCTCTTTC	TTATTCAAAT	TAATTTTTTTA	GTATGTAACA	550
TGTTAAAGGT	AAGTCTACCG	TCACTGAAAC	GTAAGACTCA	CCTCTAACTT	600
TCTATTGAGA	CAAATGCACC	ATTTTATCTG	CATTGTCTGT	AAAGATACCA	650
TCAACTCCCC	AATTAGCAAG	TTGGTTTGCA	CGTGCTGGTT	TGTTTACAGT	700
CCATACGTTT	AATTCATAAC	CCGCTTCTTT	TACCATTTTTT	ACTTTTGCTT	750
TAGTAAGTTT	GGCATCTTCA	GTGTTTACTA	TTTTAGCATT	ACAGTAATCT	800
AAAAGTGTTT	TCCAGTCTTC	ACGAAACGAA	GTTGTATGGA	ATATAACTGC	850
TCTGTTATAT	TGTGGCATGA	TTTCTTCTGC	AAGTTTAACA	AGCACACAT	900
TAAAGCTTGA	AATGAGCACT	TCTTGATTCT	GATTTAAGTT	TGTTAATTGT	950
TCTTCCACTT	GCTTAACCAT	ACTTTTAGAA	AGTGCTAGTC	CATTCGGTCC	1000
AGTAATACCT	TTTAATTCTA	CATTTAAATT	CATATTATAT	TCATTTGCTA	1050
TT					1052

2) INFORMATION FOR SEQ ID NO: 195

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3101 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*

(B) STRAIN: CCRI-9770

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195

CTTCATATGA	CGTCTATCCA	TTTATGTATG	GCATGAGTAA	CGAAGAATAT	50
AATAAAATTAA	CCGAAGATAA	AAAAGAACCT	CTGCTCAACA	AGTTCCAGAT	100
TACAACTTCA	CCAGGTTCAA	CTCAAAAAAT	ATTAACAGCA	ATGATTGGGT	150
TAAATAACAA	AACATTAGAC	GATAAAACAA	GTTATAAAAT	CGATGGTAAA	200
GGTTGGCAAA	AAGATAAATC	TTGGGGTGGT	TACAACGTTA	CAAGATATGA	250
AGTGGTAAAT	GGTAATATCG	ACTTAAACA	AGCAATAGAA	TCATCAGATA	300
ACATTTTCTT	TGCTAGAGTA	GCACTCGAAT	TAGGCAGTAA	GAAATTTGAA	350
AAAGGCATGA	AAAAACTAGG	TGTTGGTGAA	GATATACCAA	GTGATTATCC	400
ATTTTATAAT	GCTCAAATTT	CAACAAAAA	TTTAGATAAT	GAAATATTAT	450
TAGCTGATTC	AGGTTACGGA	CAAGGTGAAA	TACTGATTAA	CCCAGTACAG	500
ATCCTTTCAA	TCTATAGCGC	ATTAGAAAAA	AATGGCAATA	TTAACGCACC	550
TCACTTATTA	AAAGACACGA	AAAACAAAGT	TTGGAAGAAA	AATATTATTT	600
CCAAAGAAAA	TATCAATCTA	TTAAGTATG	GTATGCAACA	AGTCGTAAAT	650
AAAACACATA	AAGAAGATAT	TTATAGATCT	TATGCAAAC	TAATTGGCAA	700
ATCCGGTACT	GCAGAACTCA	AAATGAAACA	AGGAGAACT	GGCAGACAAA	750
TTGGGTGGTT	TATATCATAT	GATAAAGATA	ATCCAAACAT	GATGATGGCT	800
ATTAATGTTA	AAGATGTACA	AGATAAAGGA	ATGGCTAGCT	ACAATGCCAA	850
AATCTCAGGT	AAAGTGTATG	ATGAGCTATA	TGAGAACGGT	AATAAAAAAT	900
ACGATATAGA	TGAATAACAA	AACAGTGAAG	CAATCCGTAA	CGATGGTTGC	950
TTCAGTGT	TATTATGAAT	TATTAATAAG	TGCTGTTACT	TCTCCCTTAA	1000
ATACAATTTT	TTCATTTTCA	TTGTATGTTG	AAAGTGACAC	TGTAACGAGT	1050
CCATTTTCTT	TTTTTATGGA	TTTCTTATTT	GTAATTTTCA	CGATAACGTA	1100
CAATGTATTA	CCTGGGTATA	CAGGTTTAA	AAATTTAACG	TTATTCATTT	1150
GTGTTTCTGC	TACAACTTCT	TCTCCGTATT	TACCTTCTTC	TACCCATAAT	1200
TTAAATGATA	TTGAAAGTGT	ATGCATGCCA	GATGCAATGA	TACCTTTAAA	1250
TCTACTTTGT	TCTGCTTTT	CTTTATCTAT	ATGCATATAT	TGAGGATCAA	1300
AAGTTGTTGC	AAATTGGATA	ATTTCTTCTT	CTGTAATATG	AAGGCTTTT	1350
GTTTTGAATG	TTTCTCCTAC	TATAAAATCA	TCGTATTTCA	TATATGTCTC	1400
TCTTTCTTAT	TCAAATTAAT	TTTTTTAGTAT	GTAACATGTT	AAAGGTAAGT	1450
CTACCGTCAC	TGAAACGTAA	GACTCACCTC	TAACTTTCTA	TTGAGACAAA	1500
TGCACCATTT	TATCTGCATT	GTCTGTAAAG	ATACCATCAA	CTCCCCAATT	1550
AGCAAGTTGG	TTTGCACGTG	CTGGTTTGT	TACAGTCCAT	ACGTTCAATT	1600
CATAACCCGC	TTCTTTTACC	ATTTTTACTT	TTGCTTTAGT	AAGTTTGGCA	1650
TCTTCAGTGT	TTACTATTTT	AGCATTACAG	TAATCTAAAA	GTGTTCTCCA	1700
GTCTTCACGA	AACGAAGTTG	TATGGAATAT	AACGTCTCTG	TTATATTGTG	1750
GCATGATTTT	TTCTGCAAGT	TTAACAAGCA	CAACATTAAA	GCTTGAAATG	1800
AGCACTTCTT	GATTCTGATT	TAAGTTTGT	AATTGTTCTT	CCACTTGCTT	1850
AACCATACTT	TTAGAAAGTG	CTAGTCCATT	CGGTCCAGTA	ATACCTTTTA	1900
ATTCTACATT	TAAATTCATA	TTATATTCAT	TTGCTATTTT	TACTACATCA	1950
TCGAAAGTTG	GCAAATGTTC	ATCTTTGAAT	TTTTTACCAA	ACCAAGATCC	2000
TGCAGAAGCA	TCTTTAATTT	CATCATAATT	CAATTTCAGT	ATTTCCCCGG	2050
ACATATTTGT	AGTCCGTTCT	AAATAATCAT	CATGAATGAT	AATCAGTTGT	2100
TCATCTTTTG	TAATTGCAAC	ATCTAACTCC	AACAGTTTA	TACCTTCTAC	2150
TTCTGAAGCA	GCTTTAAATG	ATGCAATTGT	ATTTTCCGGA	GCTTTACTAG	2200
GTAATCCTCT	ATGTCCATAT	ACAGTTAGCA	TATTACCTCT	CCTTGCAATT	2250
TTATTTTTTT	AATTAACGTA	ACTGTATTAT	CACATTAATC	GCACTTTTAT	2300
TTCCATTAAA	AAGAGATGAA	TATCATAAAT	AAAGAAGTCG	ATAGATTCGT	2350
ATTGATTATG	GAGTTAATCT	ACGTCTCATC	TCATTTTTTA	AAAATCATT	2400
ATGTCCCAAG	CTCCATTTTG	TAATCAAGTC	TAGTTTTTCG	GTTCTGTTGC	2450
AAAGTTGAAT	TTATAGTATA	ATTTTAACAA	AAAGGAGTCT	TCTGTATGAA	2500
CTATTTTCTA	TATAAACAA	TTAACAAGGA	TGTTATCACT	GTAGCCGTTG	2550
GCTACTATCT	AAGATATACA	TTGAGTTATC	GTGATATATC	TGAAATATTA	2600
AGGGAACGTG	GTGTAAACGT	TCATCATTTCA	ACGGTCTACC	GTTGGGTTCA	2650
AGAATATGCC	CCAATTTTGT	ATCAAATTTG	GAAGAAAAAG	CATAAAAAAG	2700
CTTATTACAA	ATGGCGTATT	GATGAGACGT	ACATCAAAAT	AAAAGGAAAA	2750

TGGAGCTATT	TATATCGTGC	CATTGATGCA	GAGGGACATA	CATTAGATAT	2800
TTGGTTGCGT	AAGCAACGAG	ATAATCATTC	AGCATATGCG	TTTATCAAAC	2850
GTCTCATTAA	ACAATTTGGT	AAACCTCAAA	AGGTAATTAC	AGATCAGGCA	2900
CCTTCAACGA	AGGTAGCAAT	GGCTAAAGTA	ATTAAAGCTT	TTAAACTTAA	2950
ACCTGACTGT	CATTGTACAT	CGAAATATCT	GAATAACCTC	ATTGAGCAAG	3000
ATCACCGTCA	TATTAAAGTA	AGAAAGACAA	GGTATCAAAG	TATCAATACA	3050
GCAAAGAATA	CTTTAAAAGG	TATTGAATGT	ATTTACGCTC	TATATAAAAA	3100
G					3101

2) INFORMATION FOR SEQ ID NO: 196

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3506 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: CCRI-9887

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196

CCACCTTCAT	ATGACGTCTA	TCCATTTATG	TATGGCATGA	GTAACGAAGA	50
ATATAATAAA	TTAACC GAAG	ATAAAAAAGA	ACCTCTGCTC	AACAAGTTCC	100
AGATTACAAC	TTCACCAGGT	TCAACTCAAA	AAATATTAAC	AGCAATGATT	150
GGGTAAATA	ACAAAACATT	AGACGATAAA	ACAAGTTATA	AAATCGATGG	200
TAAAGGTTGG	CAAAAAGATA	AATCTTGGGG	TGGTTACAAC	GTTACAAGAT	250
ATGAAGTGGT	AAATGGTAAT	ATCGACTTAA	AACAAGCAAT	AGAATCATCA	300
GATAACATTT	TCTTTGCTAG	AGTAGCACTC	GAATTAGGCA	GTAAGAAATT	350
TGAAAAGGC	ATGAAAAAAC	TAGGTGTTGG	TGAAGATATA	CCAAGTGATT	400
ATCCATTTTA	TAATGCTCAA	ATTTCAAACA	AAAATTTAGA	TAATGAAATA	450
TTATTAGCTG	ATTCAGGTTA	CGGACAAGGT	GAAATACTGA	TTAACCCAGT	500
ACAGATCCTT	TCAATCTATA	GCGCATTAGA	AAATAATGGC	AATATTAACG	550
CACCTCACTT	ATTAAAAGAC	ACGAAAAACA	AAGTTTGGAA	GAAAAATATT	600
ATTTCCAAAG	AAAATATCAA	TCTATTAACT	GATGGTATGC	AACAAGTCGT	650
AAATAAAACA	CATAAAGAAG	ATATTTATAG	ATCTTATGCA	AACTTAATTG	700
GCAAATCCGG	TACTGCAGAA	CTCAAAATGA	AACAAGGAGA	AACTGGCAGA	750
CAAATTGGGT	GGTTTATATC	ATATGATAAA	GATAATCCAA	ACATGATGAT	800
GGCTATTAAT	GTTAAAGATG	TACAAGATAA	AGGAATGGCT	AGCTACAATG	850
CCAAAATCTC	AGGTAAAGTG	TATGATGAGC	TATATGAGAA	CGGTAATAAA	900
AAATACGATA	TAGATGAATA	ACAAAACAGT	GAAGCAATCC	GTAACGATGG	950
TTGCTTCACT	GTTTTATTAT	GAATTATTAA	TAAGTGCTGT	TACTTCTCCC	1000
TTAAATACAA	TTTCTTCATT	TTCATTGTAT	GTTGAAAGTG	AACTGTAAAC	1050
GAGTCCATTT	TCTTTTTTTA	TGGATTCTCT	ATTTGTAATT	TCAGCGATAA	1100
CGTACAATGT	ATTACCTGGG	TATACAGGTT	TAATAAATTT	AACGTTATTC	1150
ATTTGTGTTT	CTGCTACAAC	TTCTTCTCCG	TATTTACCTT	CTTCTACCCA	1200
TAATTTAAAT	GATATTGAAA	GTGTATGCAT	GCCAGATGCA	ATGATACCTT	1250
TAAATCTACT	TTGTTCTGCT	TTTTCTTTAT	CTATATGCAT	ATATTGAGGA	1300
TCAAAAGTTG	TTGCAAATTG	GATAATTTCT	TCTTCTGTAA	TATGAAGGCT	1350
TTTGTGTTTG	AATGTTTCTC	CTACTATAAA	ATCATCGTAT	TTCATATATG	1400
TCTCTCTTTC	TTATTCAAAT	TAATTTTTTA	GTATGTAACA	TGTTAAAGGT	1450
AAGTCTACCG	TCACTGAAAC	GTAAGACTCA	CCTCTAACTT	TCTATTGAGA	1500

CAAATGCACC	ATTTTATCTG	CATTGTCTGT	AAAGATACCA	TCAACTCCCC	1550
AATTAGCAAG	TTGGTTTGCA	CGTGCTGGTT	TGTTTACAGT	CCATACGTTT	1600
AATTCATAAC	CCGCTTCTTT	TACCATTTTT	ACTTTTGCTT	TAGTAAGTTT	1650
GGCATCTTCA	GTGTTTACTA	TTTTAGCATT	ACAGTAATCT	AAAAGTGTTT	1700
TCCAGTCTTC	ACGAAACGAA	GTTGTATGGA	ATATAACTGC	TCTGTTATAT	1750
TGTGGCATGA	TTTCTTCTGC	AAGTTTAACA	AGCACAAACAT	TAAAGCTTGA	1800
AATGAGCACT	TCTTGATTCT	GATTTAAGTT	TGTTAATTGT	TCTTCCACTT	1850
GCTTAACCAT	ACTTTTAGAA	AGTGCTAGTC	CATTTCGGTCC	AGTAATACCT	1900
TTTAATTCTA	CATTTAAATT	CATATTATAT	TCATTTGCTA	TTTTTACTAC	1950
ATCATCGAAA	GTTGGCAAAT	GTTTCATCTT	GAATTTTTC	CCAAACCAAG	2000
ATCCTGCAGA	AGCATCTTTA	ATTTTCATCAT	AATTCAATTC	AGTTATTTCC	2050
CCGGACATAT	TTGTAAGTCC	TTCTAAATAA	TCATCATGAA	TGATAATCAG	2100
TTGTTTCATCT	TTTGTAATTG	CAACATCTAA	CTCCAACCAG	TTTATACCTT	2150
CTACTTCTGA	AGCAGCTTTA	AATGATGCAA	TTGTATTTTC	CGGAGCTTTA	2200
CTAGGTAATC	CTCTATGTCC	ATATACAGTT	AGCATATTAC	CTCTCCTTGC	2250
ATTTTTATTT	TTTTAATTAA	CGTAACTGTA	TTATCACATT	AATCGCACTT	2300
TTATTTCCAT	TAAAAAGAGA	TGAATATCAT	AAATAAAGAA	GTCGATAGAT	2350
TCGTATTGAT	TATGGAGTTA	ATCTACGTCT	CATCTCATTT	TTAAAAAATC	2400
ATTTATGTCC	CAAGCTCCAT	TTTGTAATCA	AGTCTAGTTT	TTCTGTACCC	2450
CTTATCTGCA	ATTTTACTTA	GGATTGCTTT	TAACTTACCC	CTTATCAGCA	2500
ATTTTACTGA	GAAGTGCTTT	TAACGCACCT	CTTATCTGCA	ATTTTGCCTA	2550
GAAGTGCTTT	TAACGTACCT	CTTATCTGCA	ATTTTACTGA	GAAGTGCTTT	2600
TAAGTTACCC	CTTATCAGCA	ATTTTGCATG	GAATTGCTTT	TAACGTACCT	2650
CTTATCTGCA	ATTTTACTTA	GAAGTGCTTT	TAACAAACCT	CTTATCTGCA	2700
ATTTTACTTA	GAAGTGCTTT	TAACGTACCT	CTTATCTGTA	ATTTTACTGA	2750
GAAGTGCTTT	TAACAAACCT	CTTATCTGCA	ATTTTACTTA	GAAGTGCTTT	2800
TAACAAACCT	CTTATCTGCA	ATTTTACTTA	GAATTGCTTT	TACTATTCCCT	2850
CTTATTAGTA	TAATCTCAGT	AAGAATGCGT	ATAAAAAATGA	AAATTACAAC	2900
CGATTTTGTA	AGTGCTGACG	CCTGAGGGAA	TAGTATGTGC	GAGAGACTAA	2950
TGGCTCGAGC	CATACCCCTA	GGCAAGCATG	CACGTACAAA	ATCGTAAGAT	3000
AAAAAAATAA	GCATATCACT	GTAAACTTTA	AAAAATCAGT	TTAGTGATAT	3050
GCTTATTTAT	TTTCGAGTTAG	GATTTATGTC	CCAAGCTCAT	CAAGCACAAT	3100
CGGCCACTAG	TTTATTTCTC	TATCTTATAT	GTTCTGATAT	GGTCTTCTAT	3150
ACTGTATAAG	TATACTTTTG	AATATGGATC	TTGTGTCAAT	TCACGTTCTGA	3200
AATCAAATTC	TTGATTATCA	AATCTGTAA	AGAATGTTTC	GTATTCTTCG	3250
ACTGATAATT	GCTCTCTAGA	TTCTAGCATA	TTTAAGTGTT	TCTCTTTATC	3300
TAATGCTFTG	TCATATCCTT	TAACGATTGA	ACCACTAAAG	ATTTCTCCTA	3350
CTGCTCCTGA	ACCATAACTA	AATAGACATA	CTTTCTCTTC	TGGTTGGAAT	3400
GTGTGGTTCT	GTAATAACGA	AATTAACTT	AAGTATAATG	ATCCTGTATA	3450
AATGTTACCA	ACATCTCTAT	TCCATAATAC	GGTTCTGTTG	CAAAGTTGAA	3500
TTTATA					3506

2) INFORMATION FOR SEQ ID NO: 197

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 928 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*

(B) STRAIN: CCRI-175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197

TACATTAGAA	ATACAAGGAA	AGATGCTATC	TTCCGAAGGA	TTGGCCCAAG	50
AATTGAACCA	ACGCATGACC	CAAGGGCAAA	GCGACTTTGT	ATTTCGTCATT	100
GGCGGATCAA	ACGGCCTGCA	CAAGGACGTC	TTACAACGCA	GTAACCTACGC	150
ACTATCATTC	AGCAAAATGA	CATTCCCACA	TCAAATGATG	CGGGTTGTGT	200
TAATTGAACA	AGTGTACAGA	GCATTTAAGA	TTATGCGTGG	AGAAGCATAT	250
CATAAATGAT	GCGGTTTTTT	CAGCCGCTTC	ATAAAGGGAT	TTTGAATGTA	300
TCAGAACATA	TGAGGTTTAT	GTGAATTGCT	GTTATGTTTT	TAAGAAGCTT	350
ATCATAAGTA	ATGAGGTTCA	TGATTTTTGA	CATAGTTAGC	CTCCGCAGTC	400
TTTCATTTCA	AGTAAATAAT	AGCGAAATAT	TCTTTTACT	GAATACTTAT	450
AGTGAAGCAA	AGTTCCTAGCT	TTGAGAAAAT	TCTTTCTGCA	ACTAAATATA	500
GTAAATTACG	GTAAAATATA	AATAAGTACA	TATTGAAGAA	AATGAGACAT	550
AATATATTTT	ATAATAGGAG	GGAATTTCAA	ATGATAGACA	ACTTTATGCA	600
GGTCCTTAAA	TTAATTAAAG	AGAAACGTAC	CAATAATGTA	GTTAAAAAAT	650
CTGATTGGGA	TAAAGGTGAT	CTATATAAAA	CTTTAGTCCA	TGATAAGTTA	700
CCCAAGCAGT	TAAAAGTGCA	TATAAAAGAA	GATAAATATT	CAGTTGTAGG	750
GAAGGTTGCT	ACTGGGAACT	ATAGTAAAGT	TCCTTGGATT	TCAATATATG	800
ATGAGAATAT	AACAAAAGAA	ACAAAGGATG	GATATTATTT	GGTATATCTT	850
TTTCATCCGG	AAGGAGAAGG	CATATACTTA	TCTTTGAATC	AAGGATGGTC	900
AAAGATAAGT	GATATGTTTC	CGCGGGAT			928

2) INFORMATION FOR SEQ ID NO: 198

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 782 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-1262

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198

CAATGCCCAC	AGAGTTATCC	ACAAATACAC	AGGTTATACA	CTAAAAATTG	50
GGCATGAATG	TCAGAAAAAT	ATCAAAAAC	GCAAAGAATA	TTGGTATAAT	100
AAGAGGGAAC	AGTGTGAACA	AGTTAATAAC	TTGTGGATAA	CTGGAAAGTT	150
GATAACAATT	TGGAGGACCA	AACGACATGA	AAATCACCAT	TTTAGCTGTA	200
GGGAAACTAA	AAGAGAAATA	TTGGAAGCAA	GCCATAGCAG	AATATGAAAA	250
ACGTTTAGGC	CCATACACCA	AGATAGACAT	CATAGAAGTT	CCAGACGAAA	300
AAGCACCAGA	AAATATGAGC	GACAAAGAAA	TTGAGCAAGT	AAAAGAAAAA	350
GAAGGCCAAC	GAATACTAGC	CAAAATCAAA	CCACAATCAA	CAGTCATTAC	400
ATTAGAAATA	CAAGGAAAGA	TGCTATCTTC	CGAAGGATTG	GCCCAAGAAT	450
TGAACCAACG	CATGACCCAA	GGGCAAAGCG	ACTTTGTATT	CGTCATTGGC	500
GGATCAAACG	GCCTGCACAA	GGACGTCTTA	CAACGCAGTA	ACTACGCACT	550
ATCATTCAGC	AAAATGACAT	TCCCACATCA	AATGATGCGG	GTTGTGTTAA	600
TTGAACAAGT	GTACAGAGCA	TTTAAGATTA	TGCGTGGAGA	AGCGTATCAT	650
AAATAAAACT	AAAAATTAGG	TTGTGTATAA	TTTAAAAATT	TAATGAGATG	700

TGGAGGAATT	ACATATATGA	AATATTGGAT	TATACCTTGC	AATATCATAC	750
GATGTTTATA	GAGTGTTTAA	TAAACCATT	TT		782

2) INFORMATION FOR SEQ ID NO: 199

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 709 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-8894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199

TACATTAGAA	ATACAAGGAA	AGATGCTATC	TTCCGAAGGA	TTGGCCCAAG	50
AATTGAACCA	ACGCATGACC	CAAGGGCAAA	GCGACTTTGT	TTTCGTCATT	100
GGCGGATCAA	ACGGCCTGCA	CAAGGACGTC	TTACAACGCA	GTAAC TACGC	150
ACTATCATTC	AGCAAAATGA	CATTCCCACA	TCAAATGATG	CGGGTTGTGT	200
TAATTGAACA	AGTGTACAGA	GCATTTAAGA	TTATGCGAGG	AGAAGCTTAT	250
CATAAGTAAT	GAGGTTTCATG	ATTTT TGACA	TAGTTAGCCT	CCGCAGTCTT	300
TCATTTCAAG	TAAATAATAG	CGAAATATTC	TTTATACTGA	ATACTTATAG	350
TGAAGCAAAG	TTCTAGCTTT	GAGAAAATTC	TTTCTGCAAC	TAAATATAGT	400
AAATTACGGT	AAAATATAAA	TAAGTACATA	TTGAAGAAAA	TGAGACATAA	450
TATATTTTAT	AATAGGAGGG	AATTTCAAAT	GATAGACAAC	TTTATGCAGG	500
TCCTTAAATT	AATTAAAGAG	AAACGTACCA	ATAATG TAGT	TAAAAAATCT	550
GATTGGGATA	AAGGTGATCT	ATATAAAACT	TTAGTCCATG	ATAAGTTACC	600
CAAGCAGTTA	AAAGTGCATA	TAAAAGAAGA	TAAATATTCA	GTTGTAGGGA	650
AGGTTGCTAC	TGGGA ACTAT	AGTAAAGTTC	CTTGGATTTC	AATATATGAT	700
GAGAAATATA					709

2) INFORMATION FOR SEQ ID NO: 200

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200

GTGGGAAATG GCTGTTGTTG AG

22

2) INFORMATION FOR SEQ ID NO: 201

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201

TTCGTTCCCT CCATTAAGTC TC

22

2) INFORMATION FOR SEQ ID NO: 202

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202

AAAAGAAAGA CGGTGAAGGC

20

2) INFORMATION FOR SEQ ID NO: 203

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203

CACTTCATTA TACTGTTTTTC TTTGC

25

2) INFORMATION FOR SEQ ID NO: 204

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204

TCACCGTCTT TCTTTTGACC TT

22

2) INFORMATION FOR SEQ ID NO: 205

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205

TGAGATCTGC TGGAACAAAA GTGAA

25

2) INFORMATION FOR SEQ ID NO: 206

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206

CGGTCGAGTT TGCTGAAGAA

20

2) INFORMATION FOR SEQ ID NO: 207

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207

TCCCCTAATG ATAGCTGGTA TATATT

26

2) INFORMATION FOR SEQ ID NO: 208

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208

TCTAGGGAAT CAAAGAAAAG TAATAGT

27

2) INFORMATION FOR SEQ ID NO: 209

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209

CAACAARGRC AATGTGAYRT ATTATGYTGT TA

32

2) INFORMATION FOR SEQ ID NO: 210

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210

GATAAYATWG GMGAACAAGT CARAAATGG

29

2) INFORMATION FOR SEQ ID NO: 211

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211

CCRTATTGAT TGWTRACACG RCCACARTAA TTWGG

35

2) INFORMATION FOR SEQ ID NO: 212

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212

ATRTTSARTG GTTCATTTTTT GAAATAGATI CC

32

2) INFORMATION FOR SEQ ID NO: 213

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213

ACGTGTCGGT ATCTATGTWC GTGTATCAAC RG

32

2) INFORMATION FOR SEQ ID NO: 214

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214

TGTTATGRTC TACAAAACAA ACCGAYTAGC

30

2) INFORMATION FOR SEQ ID NO: 215

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215

GAWTAATAAT RGGGGAATGC TTACCTTCAG CTAT

34

2) INFORMATION FOR SEQ ID NO: 216

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216

GGTTTTTGAC TGACTTGTTT TTTACG

26

2) INFORMATION FOR SEQ ID NO: 217

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217

TAGAAYTGTT TTTTATGATT ACCRTCTTT

29

2) INFORMATION FOR SEQ ID NO: 218

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218

GGCAAAAAYA AAGACGAAGT GCTGAG

26

2) INFORMATION FOR SEQ ID NO: 219

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 721 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-9504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219

TGTAGCTTTA	GGTGAAGGGT	TAGGTCCTTC	AATAGGGGGA	ATAATAGCAC	50
ATTATATTCA	TTGGTCTTAC	CTACTTATAC	TTCCTATGAT	TACAATAGTA	100
ACTATACCTT	TTCTTATTAA	AGTAATGGTA	CCTGGTAAAT	CAACAAAAAA	150
TACATTAGAT	ATCGTAGGTA	TTGTTTTAAT	GTCTATAAGT	ATTATATGTT	200
TTATGTTATT	TACGACAAAT	TATAATTGGA	CTTTTTTAAT	ACTCTTCACA	250
ATCTTTTTTG	TGATTTTTTAT	TAAACATATT	TCAAGAGTTT	CTAACCCTTT	300
TATTAATCCT	AAACTAGGGA	AAAACATTCC	GTTTATGCTT	GGTTTGTTTT	350
CTGGTGGGCT	AATATTTTCT	ATAGTAGCTG	GTTTTATATC	AATGGTGCCT	400
TATATGATGA	AAACTATTTA	TCATGTAAAT	GTAGCGACAA	TAGGTAATAG	450

TGTTATTTTT	CCTGGAACCA	TGAGTGTTAT	TGTTTTTGGT	TATTTTGGTG	500
GTTTTTTAGT	GGATAGAAAA	GGATCATTAT	TTGTTTTTAT	TTTAGGATCA	550
TTGTCTATCT	CTATAAGTTT	TTTAACTATT	GCATTTTTTG	TTGAGTTTAG	600
TATGTGGTTG	ACTACTTTTA	TGTTTATATT	TGTTATGGGC	GGATTATCTT	650
TTACTAAAC	AGTTATATCA	AAAATAGTAT	CAAGTAGTCT	TTCTGAAGAA	700
GAAGTTGCTT	CTGGAAGAGT	T			721

2) INFORMATION FOR SEQ ID NO: 220

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1791 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: CCRI-1331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220

ATCCGGTACT	GCAGAACTCA	AAATGAAACA	AGGAGAAACT	GGCAGACAAA	50
TTGGGTGGTT	TATATCATAT	GATAAAGATA	ATCCAAACAT	GATGATGGCT	100
ATTAATGTTA	AAGATGTACA	AGATAAAGGA	ATGGCTAGCT	ACAATGCCAA	150
AATCTCAGGT	AAAGTGTATG	ATGAGCTATA	TGAGAACGGT	AATAAAAAAT	200
ACGATATAGA	TGAATAACAA	AACAGTGAAG	CAATCCGTAA	CGATGGTTGC	250
TTCAGTGT	TATTATGAAT	TATTAATAAG	TGCTGTTACT	TCTCCCTTAA	300
ATACAATTTT	TTCATTTTCA	TTGTATGTTG	AAAGTGACAC	TGTAACGAGT	350
CCATTTTCTT	TTTTTATGGA	TTTCTTATTT	GTAATTTTCA	CGATAACGTA	400
CAATGTATTA	CCTGGGTATA	CAGGTTTAAT	AAATTTAACG	TTATTCATTT	450
GTGTTCCCTGC	TACAACTTCT	TCTCCGTATT	TACCTTCTTC	TACCCATAAT	500
TTAAATGATA	TTGAAAGTGT	ATGCATGCCA	GATGCAATGA	TACCTTTAAA	550
TCTACTTTGT	TCTGCTTTTT	CTTTATCTAT	ATGCATATAT	TGAGGATCAA	600
AAGTTGTTGC	AAATTGGATA	ATTTCTTCTT	CTGTAATATG	AAGGCTTTTT	650
GTTTTGAATG	TTTCTCCTAC	TATAAAATCA	TCGTATTTC	TATATGTCTC	700
TCTTTCTTAT	TCAAATTAAT	TTTTTAGTAT	GTAACATGTT	AAAGGTAAGT	750
CTACCGTCAC	TGAAACGTAA	GACTCACCTC	TAACTTTCTA	TTGAGACAAA	800
TGCACCATTT	TATCTGCATT	GTCTGTAAAG	ATACCATCAA	CTCCCCAATT	850
AGCAAGTTGG	TTTGCACGTG	CTGGTTTGTT	TACAGTCCAT	ACGTTCAATT	900
CATAACCCGC	TTCTTTTACC	ATTTTACTTT	TTGCTTTAGT	AAGTTTGGCA	950
TCTTCAGTGT	TTACTATTTT	AGCATTACAG	TAATCTAAAA	GTGTTCTCCA	1000
GTCTTCACGA	AACGAAGTTG	TATGGAATAT	AACGTCTCTG	TTATATTGTG	1050
GCATGATTTT	TTCTGCAAGT	TTAACAAGCA	CAACATTAAA	GCTTGAAATG	1100
AGCACTTCTT	GATTCTGATT	TAAGTTTGTT	AATTGTTCTT	CCACTTGCTT	1150
AACCATACTT	TTAGAAAGTG	CTAGTCCATT	CGGTCCAGTA	ATACCTTTTA	1200
ATTCTACATT	TAAATTCATA	TTATATTTCAT	TTGCTATTTT	TACTACATCA	1250
TCGAAAGTTG	GCAAATGTTT	ATCTTTGAAT	TTTTTCACCA	ACCAAGATCC	1300
TGCAGAAGCA	TCTTTAATTT	CATCATAATT	CAATTCAGTT	ATTTCCCCGG	1350
ACATATTTGT	AGTCCGTTCT	AAATAATCAT	CATGAATGAT	AATCAGTTGT	1400
TCATCTTTTG	TAATTGCAAC	ATCTAACTCC	AACCAGTTTA	TACCTTCTAC	1450
TTCTGAAGCA	GCTTTAAATG	ATGCAATTGT	ATTTTCCGGA	GCTTTACTAG	1500
GTAATCCTCT	ATGTCCATAT	ACAGTTAGCA	TATTACCTCT	CCTTGCAATT	1550
TTATTTTTTTT	AATTAACGTA	ACTGTATTAT	CACATTAATC	GCACTTTTAT	1600

TTCCATTAAA	AAGAGATGAA	TATCATAAAT	AAAGAAGTCG	ATAGATTCGT	1650
ATTGATTATG	GAGTTAATCT	ACGTCTCATC	TCATTTTTAA	AAAATCATTT	1700
ATGTCCCAAG	CTCCATTTTG	TAATCAAGTC	TAGTTTTTCT	GTACCCCTTA	1750
TCTGCAATTT	TACTTAGGAT	TGCTTTTAAAC	TTACCCCTTA	T	1791

2) INFORMATION FOR SEQ ID NO: 221

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-1377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221

AAGTGCTGAC	GCCTGAGGGA	ATAGTATGTG	CGAGAGACTA	ATGGCTCGAG	50
CCATACCCCT	AGGCAAGCAT	GCACGTACAA	AATCGTAAGA	TAAAAAATA	100
AGCATATCAC	TGTAAACTTT	AAAAAATCAG	TTTAGTGATA	TGCTTATTTA	150
TTTCGAGTTA	GGATTTATGT	CCCAAGCTCA	TCAAGCACAA	TCGGCCACTA	200
GTTTATTTCT	CTATCTTATA	TGTTCTGATA	TGGTCTTCTA	TACTGTATAA	250
GTATACTTTT	GAATATGGAT	CTTGTGTCAA	TTCACGTTTC	AAATCAAATT	300
CTTGATTATC	AAATCTGTTA	AAGAATGTTT	CGTATTCTTC	GA CTGATAAT	350
TGCTCTCTAG	ATTCTAGCAT	ATTTAAGTGT	TTCTCTTTAT	CTAATGCTTT	400
GTCATATCCT	TTAACGATTG	AACCACTAAA	GATTTCTCCT	ACTGCTCCTG	450
AACCATAACT	AAATAGACAT	ACTTTCTCTT	CTGTTTGGAA	TGTGTGGTTC	500
TGTAATAACG	AAATTAAACT	TAAGTATAAT	GATCCTGTAT	AAATGTTACC	550
AACATCTCTA	TTCCATAATA	CGGTTCTGTT	GCAAAGTTGA	ATTTATAGTA	600

2) INFORMATION FOR SEQ ID NO: 222

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1640 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-2025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222

GGGTGGTTTA	TATCATATGA	TAAAGATAAT	CCAAACATGA	TGATGGCTAT	50
TAATGTTAAA	GATGTACAAG	ATAAAGGAAT	GGCTAGCTAC	AATGCCAAAA	100
TCTCAGGTAA	AGTGTATGAT	GAGCTATATG	AGAACGGTAA	TAAAAAATAC	150
GATATAGATG	AATAACAAAA	CAGTGAAGCA	ATCCGTAAACG	ATGGTTGCTT	200
CACTGTTTTA	TTATGAATTA	TTAATAAGTG	CTGTTACTTC	TCCCTTAAAT	250
ACAATTTCTT	CATTTTCATT	GTATGTTGAA	AGTGACACTG	TAACGAGTCC	300
ATTTTCTTTT	TTTATGGATT	TCTTATTTGT	AATTTTCAGCG	ATAACGTACA	350
ATGTATTACC	TGGGTATACA	GGTTTAATAA	ATTTAACGTT	ATTCATTTGT	400
GTTCTTGCTA	CAACTTCTTC	TCCGTATTTA	CCTTCTTCTA	CCCATAATTT	450
AAATGATATT	GAAAGTGTAT	GCATGCCAGA	TGCAATGATA	CCTTTAAATC	500
TACTTTGTTT	TGCTTTTTTCT	TTATCTATAT	GCATATATTG	AGGATCAAAA	550
GTTGTTGCAA	ATTGGATAAT	TTCTTCTTCT	GTAATATGAA	GGCTTTTTTGT	600
TTTGAATGTT	TCTCCTACTA	TAAAAATCATC	GTATTTTCATA	TATGTCCTCTC	650
TTTCTTATTC	AAATTAATTT	TTTAGTATGT	AACATGTTAA	AGGTAAGTCT	700
ACCGTCACTG	AAACGTAAAG	CTCACCTCTA	ACTTTCCTATT	GAGACAAATG	750
CACCATTTTA	TCTGCATTGT	CTGTAAAGAT	ACCATCAACT	CCCCAATTAG	800
CAAGTTGGTT	TGCACGTGCT	GGTTTGTTTA	CAGTCCATAC	GTTCAATTCA	850
TAACCCGCTT	CTTTTACCAT	TTTTACTTTT	GCTTTAGTAA	GTTTGGCATC	900
TTCAGTGTTT	ACTATTTTAG	CATTACAGTA	ATCTAAAAGT	GTTCTCCAGT	950
CTTCACGAAA	CGAAGTTGTA	TGGAATATAA	CTGCTCTGTT	ATATTGTGGC	1000
ATGATTTCTT	CTGCAAGTTT	AACAAGCACA	ACATTAAAGC	TTGAAATGAG	1050
CACTTCTTGA	TTCTGATTTA	AGTTTGTTAA	TTGTTCTTCC	ACTTGCTTAA	1100
CCATACTTTT	AGAAAGTGCT	AGTCCATTCT	GTCCAGTAAT	ACCTTTTAAT	1150
TCTACATTTA	AATTCATATT	ATATTCATTT	GCTATTTTAA	CTACATCATC	1200
GAAAGTTGGC	AAATGTTTCAT	CTTTGAATTT	TTCACCAAAC	CAAGATCCTG	1250
CAGAAGCATC	TTTAATTTCA	TCATAATTCA	ATTGAGTTAT	TTCCCCGGAC	1300
ATATTTGTAG	TCCGTTCTAA	ATAATCATCA	TGAATGATAA	TCAGTTGTTT	1350
ATCTTTTGTA	ATTGCAACAT	CTAACTCCAA	CCAGTTTATA	CCTTCTACTT	1400
CTGAAGCAGC	TTTAAATGAT	GCAATTGTAT	TTTCCGGAGC	TTTACTAGGT	1450
AATCCTCTAT	GTCCATATAC	AGTTAGCATA	TTACCTCTCC	TTGCATTTTT	1500
ATTTTTTTAA	TTAACGTAAC	TGTATTATCA	CATTAATCGC	ACTTTTATTT	1550
CCATTAAAAA	GAGATGAATA	TCATAAATAA	AGAAGTCGAT	AGATTTCGTAT	1600
TGATTATGGA	GTTAATCTAC	GTCTCATCTC	ATTTTTAAAA		1640

2) INFORMATION FOR SEQ ID NO: 223

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 592 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-2025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223

AATTCAACTT	TGCAACAGAA	CCGTATTATG	GAATAGAGAT	GTTGGTAACA	50
TTTATACAGG	ATCATTATAC	TTAAGTTTAA	TTTCGTTATT	ACAGAACCAC	100
ACATTCCAAC	CAGAAGAGAA	AGTATGTCTA	TTTAGTTATG	GTTCAGGAGC	150
AGTAGGAGAA	ATCTTTAGTG	GTTCAATCGT	TAAAGGATAT	GACAAAGCAT	200
TAGATAAAGA	GAAACACTTA	AATATGCTAG	AATCTAGAGA	GCAATTATCA	250

GTCGAAGAAT	ACGAAACATT	CTTTAACAGA	TTTGATAATC	AAGAATTTGA	300
TTTCGAACGT	GAATTGACAC	AAGATCCATA	TTCAAAAAGTA	TACTTATACA	350
GTATAGAAGA	CCATATCAGA	ACATATAAGA	TAGAGAAATA	AACTAGTGGC	400
CGATTGTGCT	TGATGAGCTT	GGGACATAAA	TCCTAACTCG	AAATAAATAA	450
GCATATCACT	AAACTGATTT	TTTAAAGTTT	ACAGTGATAT	GCTTATTTTT	500
TTATCTTACG	ATTTTGTACG	TGCATGCTTG	CCTAGGGGTA	TGGCTCGAGC	550
CATTAGTCTC	TCGCACATAC	TATTCCCTCA	GGCGTCAGCA	CT	592

2) INFORMATION FOR SEQ ID NO: 224

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2386 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: CCRI-9860

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224

CACCTTCATA	TGACGTCTAT	CCATTTATGT	ATGGCATGAG	TAACGAAGAA	50
TATAATAAAT	TAACCGAAGA	TAAAAAAGAA	CCTCTGCTCA	ACAAGTTCCA	100
GATTACAAC	TCACCAGGTT	CAACTCAAAA	AATATTAACA	GCAATGATTG	150
GGTTAAATAA	CAAAACATTA	GACGATAAAA	CAAGTTATAA	AATCGATGGT	200
AAAGGTTGGC	AAAAAGATAA	ATCTTGGGGT	GGTTACAACG	TTACAAGATA	250
TGAAGTGTA	AATGGTAATA	TCGACTTAAA	ACAAGCAATA	GAATCATCAG	300
ATAACATTTT	CTTTGCTAGA	GTAGCACTCG	AATTAGGCAG	TAAGAAATTT	350
GAAAAAGGCA	TGAAAAAACT	AGGTGTTGGT	GAAGATATAC	CAAGTGATTA	400
TCCATTTTAT	AATGCTCAAA	TTTCAAACAA	AAATTTAGAT	AATGAAATAT	450
TATTAGCTGA	TTCAGGTTAC	GGACAAGGTG	AAATACTGAT	TAACCCAGTA	500
CAGATCCTTT	CAATCTATAG	CGCATTAGAA	AATAATGGCA	ATATTAACGC	550
ACCTCACTTA	TTAAAAGACA	CGAAAAACAA	AGTTTGGAAG	AAAAATATTA	600
TTTCCAAAGA	AAATATCAAT	CTATTAAGTG	ATGGTATGCA	ACAAGTCGTA	650
AATAAAACAC	ATAAAGAAGA	TATTTATAGA	TCTTATGCAA	ACTTAATTGG	700
CAAATCCGGT	ACTGCAGAAC	TCAAATGAA	ACAAGGAGAA	ACTGGCAGAC	750
AAATTGGGTG	GTTTATATCA	TATGATAAAG	ATAATCCAA	CATGATGATG	800
GCTATTAATG	TTAAAGATGT	ACAAGATAAA	GGAATGGCTA	GCTACAATGC	850
CAAAATCTCA	GGTAAAGTGT	ATGATGAGCT	ATATGAGAAC	GGTAATAAAA	900
AATACGATAT	AGATGAATAA	CAAAACAGTG	AAGCAATCCG	TAACGATGGT	950
TGCTTCACTG	TTTTATTATG	AATTATTAAT	AAGTGCTGTT	ACTTCTCCCT	1000
TAAATACAAT	TTCTTCATTT	TCATTGTATG	TTGAAAGTGA	CACTGTAACG	1050
AGTCCATTTT	CTTTTTTTTAT	GGATTTCTTA	TTTGTAATTT	CAGCGATAAC	1100
GTACAATGTA	TTACCTGGGT	ATACAGGTTT	AATAAATTTA	ACGTTATTCA	1150
TTTGTGTTCC	TGCTACAAC	TCTTCTCCGT	ATTTACCTTC	TTCTACCCAT	1200
AATTTAAATG	ATATTGAAAG	TGTATGCATG	CCAGATGCAA	TGATACCTTT	1250
AAATCTACTT	TGTTCTGCTT	TTTCTTTATC	TATATGCATA	TATTGAGGAT	1300
CAAAAGTTGT	TGCAAATTGG	ATAATTTCTT	CTTCTGTAAT	ATGAAGGCTT	1350
TTTGTTTTGA	ATGTTTCTCC	TACTATAAAA	TCATCGTATT	TCATATATGT	1400
CTCTCTTTCT	TATTCAAATT	AATTTTTTAG	TATGTAACAT	GTTAAAGGTA	1450
AGTCTACCGT	CACTGAAACG	TAAGACTCAC	CTCTAACTTT	CTATTGAGAC	1500
AAATGCACCA	TTTTATCTGC	ATTGTCTGTA	AAGATACCAT	CAACTCCCCA	1550

ATTAGCAAGT	TGGTTTGCAC	GTGCTGGTTT	GTTTACAGTC	CATACGTTCA	1600
ATTCATAACC	CGCTTCTTTT	ACCATTTTTT	CTTTTGCTTT	AGTAAGTTTG	1650
GCATCTTCAG	TGTTTACTAT	TTTAGCATT	CAGTAATCTA	AAAGTGTTCT	1700
CCAGTCTTCA	CGAAACGAAG	TTGTATGGAA	TATAACTGCT	CTGTTATATT	1750
GTGGCATGAT	TTCTTCTGCA	AGTTTAAACAA	GCACAACATT	AAAGCTTGAA	1800
ATGAGCACTT	CTTGATTCTG	ATTTAAGTTT	GTTAATTGTT	CTTCCACTTG	1850
CTTAACCATA	CTTTTAGAAA	GTGCTAGTCC	ATTCGGTCCA	GTAATACCTT	1900
TTAATTCTAC	ATTTAAATTC	ATATTATATT	CATTTGCTAT	TTTTACTACA	1950
TCATCGAAAG	TTGGCAAATG	TTCATCTTTG	AATTTTTCAC	CAAACCAAGA	2000
TCCTGCAGAA	GCATCTTTAA	TTTCATCATA	ATTCAATTCA	GTTATTTCCC	2050
CGGACATATT	TGTAGTCCGT	TCTAAATAAT	CATCATGAAT	GATAATCAGT	2100
TGTTCATCTT	TTGTAATTGC	AACATCTAAC	TCCAACCAGT	TTATACCTTC	2150
TACTTCTGAA	GCAGCTTTAA	ATGATGCAAT	TGTATTTTCC	GGAGCTTTAC	2200
TAGGTAATCC	TCTATGTCCA	TATACAGTTA	GCATATTACC	TCTCCTTGCA	2250
TTTTTATTTT	TTTAATTAAC	GTAACGTGAT	TATCACATTA	ATCGCACTTT	2300
TATTTCCATT	AAAAAGAGAT	GAATATCATA	AATAAAGAAG	TCGATAGATT	2350
CGTATTGATT	ATGGAGTTAA	TCTACGTCTC	ATCTCA		2386

2) INFORMATION FOR SEQ ID NO: 225

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 623 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-9860

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225

TGAAAATTAC	AACCGATTTT	GTAAGTGCTG	ACGCCTGAGG	GAATAGTATG	50
TGCGAGAGAC	TAATGGCTCG	AGCCATACCC	CTAGGCAAGC	ATGCACGTAC	100
AAAATCGTAA	GATAAAAAAA	TAAGCATATC	ACTGTAAACT	TTAAAAAATC	150
AGTTTAGTGA	TATGCTTATT	TATTTTCGAGT	TAGGATTTAT	GTCCCAAGCT	200
CATCAAGCAC	AATCGGCCAC	TAGTTTATTT	CTCTATCTTA	TATGTTCTGA	250
TATGGTCTTC	TATACTGTAT	AAGTATACTT	TTGAATATGG	ATCTTGTGTC	300
AATTCACGTT	CGAAATCAAA	TTCTTGATTA	TCAAATCTGT	TAAAGAATGT	350
TTCGTATTCT	TCGACTGATA	ATTGCTCTCT	AGATTCTAGC	ATATTTAAGT	400
GTTTCTCTTT	ATCTAATGCT	TTGTCATATC	CTTTAACGAT	TGAACCACTA	450
AAGATTTCTC	CTACTGCTCC	TGAACCATAA	CTAAATAGAC	ATACTTTCTC	500
TTCTGGTTGG	AATGTGTGGT	TCTGTAATAA	CGAAATTAAA	CTTAAGTATA	550
ATGATCCTGT	ATAAATGTTA	CCAACATCTC	TATTCCATAA	TACGGTTCTG	600
TTGCAAAGTT	GAATTTATAG	TAT			623

2) INFORMATION FOR SEQ ID NO: 226

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (C) ACCESSION NUMBER: Extracted from L29436

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226

ATGAAAAATA	TTTCAGAATT	CTCAGCCCCAA	CTTGATCAAA	CTTTTGATCA	50
AGGGGAAGCC	GTCTCTATGG	AGTGGTTATT	CCGTCCGTTG	CTAAAAATGC	100
TGGCGGAGGG	CGATCCAGTC	CCC GTTGAGG	ACATCGCGGC	GGAGACCGGG	150
AAGCCCGTCG	AGGAAGTTAA	GCAAGTCCTA	CAGACTCTAC	CTAGTGTGGA	200
ACTTGATGAG	CAGGGCCGTG	TCGTGCGTTA	TGGCCTCACA	CTGTTCCCTA	250
CCCCCATCG	CTTCGAGGTT	GATGGGAAGC	AACTATATGC	ATGGTGCGCC	300
CTTGACACAC	TTATGTTCCC	AGCACTCATC	GGCCGGACGG	TCCACATCGC	350
TTCGCCTTGT	CACGGCACCG	GTAAGTCCGT	CCGTTTGACG	GTGGAACCGG	400
ACCGCGTTGT	AAGCGTCGAG	CCTTCAACAG	CCGTTGTCTC	GATTGTTACA	450
CCAGATGAAA	TGGCCTCGGT	TCGGTCGGCC	TTCTGTAAACG	ACGTTCACTT	500
TTTCAGTTCA	CCGAGTGCAG	CCCAAGACTG	GCTTAACCAA	CACCCTGAGT	550
CGAGCGTTTT	GCCCGTTGAA	GATGCCTTTG	AACTGGGTCG	CCATTTGGGA	600
GCGCGTTATG	AGGAGTCAGG	ACCTACTAAT	GGGTCCTGTT	GTAACATTTA	650
A					651

2) INFORMATION FOR SEQ ID NO: 227

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 563 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (C) ACCESSION NUMBER: Extracted from L29436

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227

ATGAATCTTG	AAAAAGGGAA	TATAGAAAGG	AAAAAACATG	GTGTCCATGT	50
TAATGAGTAT	TTGCAAAGTG	TAAGTAACCC	GAATGTCTAT	GCAGCTGGAG	100
ATGCTGCAGC	AACGGATGGC	TTGCCCTCA	CACCTGTAGC	CAGTGCAGAT	150
TCTCATGTCTG	TAGCATCTAA	TTTATTGAAA	GGGAACAGCA	AAAAAATTGA	200
ATATCCCGTG	ATTCCATCTG	CTGTATTTAC	CGTACCTAAA	ATGGCATCGG	250
TAGGTATGAG	CGAGGAGGAA	GCCAAAAACT	CTGGCCGGAA	TATTAAAGTA	300
AAGCAGAAAA	ACATCTCCGA	CTGGTTTACG	TATAAACGGA	CAAATGAGGA	350
CTTTGCTGCG	TTTAAAGTGC	TGATTGACGA	AGATCATGAT	CAAATTGTTG	400
GTGCTCATTT	GATTAGTAAT	GAAGCCGATG	AACTGATTAA	TCATTTTGCA	450
ACAGCCATTC	GTTTTGGGAT	TTCAACCAAA	GAATTGAAAC	AAATGATATT	500

TGCCTATCCA	ACGGCAGCTT	CGGACATTGC	ACACATGTTG	TAAGTTTGCG	550
TTTTGTGAGA	TGT				563

2) INFORMATION FOR SEQ ID NO: 228

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1380 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (C) ACCESSION NUMBER: Extracted from S67449

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228

TTGTTTAGTT	TATATAAAAA	ATTTAAAGGT	TTGTTTTTATA	GCGTTTTTATT	50
TTGGCTTTGT	ATTCTTTCAT	TTTTTAGTGT	ATTAAATGAA	ATGGTTTTTAA	100
ATGTTTCTTT	ACCTGATATT	GCAAATCATT	TTAATACTAC	TCCTGGAATT	150
ACAAACTGGG	TAAACACTGC	ATATATGTTA	ACTTTTTTCG	TAGGAACAGC	200
AGTATATGGA	AAATTATCTG	ATTATATAAA	TATAAAAAAA	TTGTTAATTA	250
TTGGTATTAG	TTTGAGCTGT	CTTGGTTCAT	TGATTGCTTT	TATTGGTCAC	300
AATCACTTTT	TTATTTTGAT	TTTTGGTAGG	TTAGTACAAG	GAGTAGGATC	350
TGCTGCATTC	CCTTCACTGA	TTATGGTGGT	TGTAGCTAGA	AATATTACAA	400
GAAAAAACA	AGGCAAAGCC	TTTGGTTTTA	TAGGATCAAT	TGTAGCTTTA	450
GGTGAAGGGT	TAGGTCCTTC	AATAGGGGGA	ATAATAGCAC	ATTATATTCA	500
TTGGTCTTAC	CTACTTATAC	TTCCTATGAT	TACAATAGTA	ACTATACCTT	550
TTCTTATTAA	AGTAATGGTA	CCTGGTAAAT	CAACAAAAAA	TACATTAGAT	600
ATCGTAGGTA	TTGTTTTAAT	GTCTATAAGT	ATTATATGTT	TTATGTTATT	650
TACGACAAAT	TATAATTGGA	CTTTTTTAAT	ACTCTTCACA	ATCTTTTTTG	700
TGATTTTTAT	TAAACATATT	TCAAGAGTTT	CTAACCCCTT	TATTAATCCT	750
AAACTAGGGA	AAAACATTCC	GTTTATGCTT	GGTTTGTTTT	CTGGTGGGCT	800
AATATTTTCT	ATAGTAGCTG	GTTTTATATC	AATGGTGCCT	TATATGATGA	850
AACTATTTA	TCATGTAAAT	GTAGCGACAA	TAGGTAATAG	TGTTATTTTT	900
CCTGGAACCA	TGAGTGTTAT	TGTTTTTGTT	TATTTTGGTG	GTTTTTTTAGT	950
GGATAGAAAA	GGATCAATTAT	TTGTTTTTAT	TTTAGGATCA	TTGTCTATCT	1000
CTATAAGTTT	TTTAACCTATT	GCATTTTTTG	TTGAGTTTAG	TATGTGGTTG	1050
ACTACTTTTA	TGTTTATATT	TGTTATGGGC	GGATTATCTT	TTACTAAAAC	1100
AGTTATATCA	AAAATAGTAT	CAAGTAGTCT	TTCTGAAGAA	GAAGTTGCTT	1150
CTGGAATGAG	TTTGCTAAAT	TTCACAAGTT	TTTTATCAGA	GGGAACAGGT	1200
ATAGCAATTG	TAGGAGGTTT	ATTGTCACTA	CAATTGATTA	ATCGTAAACT	1250
AGTTCTGGAA	TTTATAAATT	ATTCTTCTGG	AGTGTATAGT	AATATTCTTG	1300
TAGCCATGGC	TATCCTTATT	ATTTTATGTT	GTCTTTTGAC	GATTATTGTA	1350
TTTAAACGTT	CTGAAAAGCA	GTTTGAATAG			1380

2) INFORMATION FOR SEQ ID NO: 229

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1365 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: HUC19
- (C) ACCESSION NUMBER: Extracted from AF181950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229

ATGAGAATAG	TGAATGGACC	AATAATAATG	ACTAGAGAAG	AAAGAATGAA	50
GATTGTTTCAT	GAAATTAAGG	AACGAATATT	GGATAAATAT	GGGGATGATG	100
TTAAGGCTAT	TGGTGTTTAT	GGCTCTCTTG	GTCGTCAGAC	TGATGGGCCC	150
TATTCGGATA	TTGAGATGAT	GTGTGTCATG	TCAACAGAAG	AAGCAGAGTT	200
CAGCCATGAA	TGGACAACCG	GTGAGTGGAA	GGTGGAAGTG	AATTTTGTATA	250
GCGAAGAGAT	TCTACTAGAT	TATGCATCTC	AGGTGGAATC	AGATTGGCCT	300
CTTACACATG	GTCAATTTTT	CTCTATTTTG	CCGATTTATG	ATTCAGGTGG	350
ATACTTAGAG	AAAGTGTATC	AAACTGCTAA	ATCGGTAGAA	GCCCAAACGT	400
TCCACGATGC	GATTTGTGCC	CTTATCGTAG	AAGAGCTGTT	TGAATATGCA	450
GGCAAATGGC	GTAATATTTCG	TGTGCAAGGA	CCGACAACAT	TTCTACCATC	500
CTTGACTGTA	CAGGTAGCAA	TGGCAGGTGC	CATGTTGATT	GGTCTGCATC	550
ATCGCATCTG	TTATACGACG	AGCGCTTCGG	TCTTAACTGA	AGCAGTTAAG	600
CAATCAGATC	TTCTTCAGG	TTATGACCAT	CTGTGCCAGT	TCGTAATGTC	650
TGGTCAACTT	TCCGACTCTG	AGAACTTCT	GGAATCGCTA	GAGAATTTCT	700
GGAATGGGAT	TCAGGAGTGG	ACAGAACGAC	ACGGATATAT	AGTGGATGTG	750
TCAAAACGCA	TACCATTTTG	AACGATGACC	TCTAATAATT	GTTAATCATG	800
TTGGTTACGT	TTTATTAAAC	TTCTCCTAGT	ATTAGTAATT	ATCATGGCTG	850
TCATGGCGCA	TTAACGGAAT	AAAGGGTGTG	CTTAAATCGG	GCCATTTTGC	900
GTAATAAGAA	AAAGGATTAA	TTATGAGCGA	ATTGAATTAA	TAATAAGGTA	950
ATAGATTTAC	ATTAGAAAAT	GAAAGGGGAT	TTTATGCGTG	AGAATGTTAC	1000
AGTCTATCCC	GGCATTGCCA	GTCGGGGATA	TTAAAAAGAG	TATAGGTTTT	1050
TATTGCGATA	AACTAGGTTT	CACTTTGGTT	CACCATGAAG	ATGGATTCGC	1100
AGTTCTAATG	TGTAATGAGG	TTCGGATTCA	TCTATGGGAG	GCAAGTGATG	1150
AAGGCTGGCG	CTCTCGTAGT	AATGATTAC	CGGTTTGTAC	AGGTGCGGAG	1200
TCGTTTATTG	CTGGTACTGC	TAGTTGCCGC	ATTGAAGTAG	AGGGAATTGA	1250
TGAATTATAT	CAACATATTA	AGCCTTTGGG	CATTTTGCAC	CCCAATACAT	1300
CATTAAAGA	TCAGTGGTGG	GATGAACGAG	ACTTTGCAGT	AATTGATCCC	1350
GACAACAATT	TGATT				1365

2) INFORMATION FOR SEQ ID NO: 230

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: HUC19
 (C) ACCESSION NUMBER: Extracted from AF181950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230

ATGGGGGTTT	CTTTTAATAT	TATGTGTCCT	AATAGTAGCA	TTTATTCAGA	50
TGAAAAATCA	AGGGTTTTAG	TGGACAAGAC	AAAGAGTGGA	AAAGTGAGAC	100
CATGGAGAGA	AAAGAAAATC	GCTAATGTTG	ATTACTTTGA	ACTTCTGCAT	150
ATTCTTGAAT	TAAAAAAGGC	TGAAAGAGTA	AAAGATTGTG	CTGAAATATT	200
AGAGTATAAA	CAAAATCGTG	AAACAGGCGA	AAGAAAGTTG	TATCGAGTGT	250
GGTTTTGTAA	ATCCAGGCTT	TGTCCAATGT	GCAACTGGAG	GAGAGCAATG	300
AAACATGGCA	TTCAGTCACA	AAAGGTTGTT	GCTGAAGTTA	TTAAACAAAA	350
GCCAACAGTT	CGTTGGTTGT	TTCTCACATT	AACAGTTAAA	AATGTTTATG	400
ATGGCGAAGA	ATTAAATAAG	AGTTTGTCTCAG	ATATGGCTCA	AGGATTTCTGC	450
CGAATGACGC	AATATAAAAA	AATTAATAAA	AATCTTGTTG	GTTTTATGCG	500
TGCAACGGAA	GTGACAATAA	ATAATAAAGA	TAATTCTTAT	AATCAGCACA	550
TGCATGTATT	GGTATGTGTG	GAACCAACTT	ATTTTAAGAA	TACAGAAAAC	600
TACGTGAATC	AAAAACAATG	GATTCAATTT	TGGAAAAAGG	CAATGAAATT	650
AGACTATGAT	CCAAATGTAA	AAGTTCAAAT	GATTTCGACCG	AAAAATAAAT	700
ATAAATCGGA	TATACAATCG	GCAATTGACG	AAACTGCAAA	ATATCCTGTA	750
AAGGATACGG	ATTTTATGAC	CGATGATGAA	GAAAAGAATT	TGTAACGTTT	800
GTCTGATTTG	GAGGAAGGTT	TACACCGTAA	A		831

2) INFORMATION FOR SEQ ID NO: 231

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4193 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: N315
 (C) ACCESSION NUMBER: Extracted from AP003129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231

ATGAGCCGCT	TGATACGCAT	GAGTGTATTA	GCAAGTGGTA	GTACAGGTAA	50
CGCCACTTTT	GTAGAAAATG	AAAAAGGTAG	TCTATTAGTT	GATGTTGGTT	100
TGACTGGCAA	GAAAATGGAA	GAATTGTTTA	GTCAAATTGA	CCGTAATATT	150
CAAGATTTAA	ATGGTATTTT	AGTAACCCAT	GAACATATTG	ATCATATTAA	200
AGGATTAGGT	GTTTTGGCGC	GTAAATATCA	ATTGCCAATT	TATGCGAATG	250
AAAAGACTTG	GCAGGCAATT	GAAAAGAAAG	ATAGTCGCAT	CCCTATGGAT	300
CAGAAATTCA	TTTTTAATCC	TTATGAAACA	AAATCTATTG	CAGGTTTCTGA	350
TGTTGAATCG	TTTAACGTGT	CACATGATGC	AATAGATCCG	CAATTTTATA	400
TTTTCCATAA	TAACATAAG	AAGTTTACGA	TTTTAACGGA	TACGGGTTAC	450
GTGTCTGATC	GTATGAAAGG	TATGATACGT	GGCAGCGATG	CGTTTATTTT	500
TGAGAGTAAT	CATGACGTCG	ATATGTTGAG	AATGTGTCTG	TATCCATGGA	550
AGACGAAACA	ACGTATTTTA	GGCGATATGG	GTCATGTATC	TAATGAGGAT	600
GCGGGTCATG	CGATGACAGA	TGTGATTACA	GGTAACACGA	AACGTATTTA	650

CCTATCGCAT	TTATCACAAG	ACAATAACAT	GAAAGATTTG	GCGCGTATGA	700
GTGTTGGCCA	AGTATTGAAC	GAACACGATA	TTGATACGGA	AAAAGAAGTA	750
TTGCTATGTG	ATACGGATAA	AGCTATTCCA	ACGCCAATAT	ATACAATATA	800
AATGAGAGTC	ACCCTATAAA	GTTCTGGCACT	GCTGTGAGAC	GACTTTATCG	850
GGTGCTTTTT	TATGTTATTG	GTGGGAAATG	GCTGTTGTTG	GAATTAAGGT	900
TCTATTTGAA	ATGTAAAAAA	TAATTCGATA	TTAAATGTAA	TTTATAAATA	950
ATTTACATAA	AATCAATCAT	TTTAATATAA	GGATTATGAT	AATATATTGG	1000
TGTATGACAG	TTAATGGAGG	GAACGAAATG	AAAGCTTTAT	TACTTAAAC	1050
AAGTGTATGG	CTCGTTTTGC	TTTTTAGTGT	GATGGGATTA	TGGCAAGTCT	1100
CGAACGCGGC	TGAGCAGTAT	ACACCAATCA	AAGCACATGT	AGTAACAACG	1150
ATAGACAAAG	CAACAACAGA	TAAGCAACAA	GTAACGCCAA	CAAAGGAAGC	1200
GGCTCATCAA	TTTGGTGAAG	AAGCGGCAAC	CAACGTATCA	GCATCAGCAC	1250
AGGGAACAGC	TGATGAAATA	AACAATAAAG	TAACATCCAA	CGCATTTTCT	1300
AACAAACCAT	CTACAGCAGT	TTCAACAAAA	GTAAACGAAA	CGCACGATGT	1350
AGATACACAA	CAAGCCTCAA	CACAAAAACC	AACTCAATCA	GCAACATTCA	1400
CATTATCAAA	TGCTAAAACA	GCATCACTTT	CACCACGAAT	GTTTGCTGCC	1450
AATGTACCAC	AAACAACAAC	ACATAAAATA	TTACATACAA	ATGATATCCA	1500
TGGCCGACTA	GCCGAAGAAA	AAGGGCGTGT	CATCGGTATG	GCTAAATTAA	1550
AAACAATAAA	AGAACAAGAA	AAGCCTGATT	TAATGTTAGA	CGCAGGAGAC	1600
GCCTTCCAAG	GTTTACCACT	TTCAAACCAG	TCTAAAGGTG	AAGAAATGGC	1650
TAAAGCAATG	AATGCAGTAG	GTTATGATGC	TATGGCAGTG	GGTAACCATG	1700
AATTTGACTT	TGGATACGAT	CAGTTGAAAA	AGTTAGAGGG	TATGTTAGAC	1750
TTCCCGATGC	TAAGTACTAA	CGTTTACAAA	GATGGGAAAC	GCGCGTTTAA	1800
GCCTTCAACA	ATTGTAACGA	AAAATGGTAT	TCGTTATGGA	ATTATTGGCG	1850
TAACGACACC	AGAAACAAAG	ACGAAAACAA	GACCTGAGGG	CATTAAAGGT	1900
GTTGAATTTA	GAGATCCATT	ACAAAGTGTG	ACAGCAGAAA	TGATGCGTAT	1950
TTATAAAGAC	GTAGATACAT	TTGTTGTTAT	ATCACATTTA	GGGATTGATC	2000
CTTCAACACA	AGAAACATGG	CGTGGTGATT	ACTTAGTGAA	ACAATTAAGT	2050
CAAAATCCAC	AATTGAAGAA	ACGTATTACA	GTCATTGATG	GTCATTACAA	2100
TACCGTACTT	CAAAATGGTC	AAATTTATAA	CAATGATGCA	TTAGCACAAA	2150
CAGGTACAGC	ACTTGCGAAT	ATCGGTAAAG	TTACATTTAA	TTACCGCAAT	2200
GGAGAGGTAT	CAAATATTAA	ACCGTCATTG	ATTAATGTTA	AAGACGTTGA	2250
AAATGTAAAC	CCGAACAAAG	CATTAGCTGA	ACAAATTAAT	CAAGCTGATC	2300
AAACATTTAG	AGCACAAACA	GCAGAGGTTA	TTATTCCTAA	TAATACCATT	2350
GATTTCAAAG	GAGAAAGAGA	TGACGTTAGA	ACGCGTGAAA	CAAATTTAGG	2400
AAACGCGATT	GCAGATGCTA	TGGAAGCGTA	TGGCGTTAAG	AATTTCTCTA	2450
AAAAGACTGA	CTTTGCCGTG	ACAAATGGTG	GAGGTATTCT	TGCCTCTATC	2500
GCAAAAGGTA	AGGTGACACG	CTATGATTTA	ATCTCAGTAT	TACCATTTGG	2550
AAATACGATT	GCGCAAATTG	ATGTAAAAGG	TTCAGACGTC	TGGACAGCTT	2600
TCGAACATAG	TTTAGGTGCA	CCAACAACAC	AAAAAGACGG	TAAGACAGTA	2650
TTAACAGCGA	ATGGCGGTTT	ACTACATATC	TCTGATTCAA	TTCGTGTTTA	2700
CTATGATATG	AATAAACCGT	CTGGCAAACG	AATTAACGCT	ATTCAAATTT	2750
TAAATAAAGA	GACAGGTAAG	TTTGAAAATA	TTGATTTAAA	ACGTGTATAT	2800
CATGTAACGA	TGAATGACTT	CACAGCATCA	GGTGGCGACG	GATATAGTAT	2850
GTTCCGTGGC	CCTAGAGAAG	AAGGTATTTT	ATTAGATCAA	GTAAGTACAA	2900
GTTATTTAAA	AACAGCTAAC	ATAGCTAAGT	ATGATACGAC	AGAACCACAA	2950
CGTATGTTAT	TAGGTAAACC	AGCAGTAAGT	GAACAACCAG	CTAAAGGACA	3000
ACAAGGTAGC	AAAGGTAGTG	AGTCTGGTAA	AGATGTACAA	CCAATTGGTG	3050
ACGACAAAGC	GATGAATCCA	GCGAAACAAC	CAGCGACAGG	TAAAGTTGTA	3100
TTGTTACCAA	CGCATAGAGG	AACGTGTTAGT	AGCGGTACAG	AAGGTTCTGG	3150
TCGCACATTA	GAAGGAGCTA	CTGTATCAAG	CAAGAGTGGG	AACCAATTGG	3200
TTAGAATGTC	AGTGCCTAAA	GGTAGCGCGC	ATGAGAAACA	GTTACCAAAA	3250
ACTGGAACCTA	ATCAAAGCTC	AAGCCCAGCA	GCGATGTTTG	TATTAGTAGC	3300
AGGTATAGGT	TTAATCGCGA	CTGTACGACG	TAGAAAAGCT	AGTTAAAATA	3350
TATTGAAAAC	AATACTACTG	TATTTCTTAA	ATAAGAGGTA	CGGTAGTGTT	3400
TTTTTATGGA	AAAAAGCTAT	AAACGTTGAT	AAACATGGGA	TATAAAAACG	3450
GGGATAAGTA	ATAAGACATC	AAGGTGTTTA	TCCACAGAAA	TGGGGATAGT	3500
TATCCAGAAT	TGTGTACAAT	TTAAAGAGAA	ATACCCACAA	TGCCCACAGA	3550

GTTATCCACA	AATACACAAG	TTATACACTA	AAAATTGGGC	ATAAATGTCA	3600
GGAAAATATC	AAAAACTGCA	AAAAATATTG	GTATAATAAG	AGGGAACAGT	3650
GTGAACAAGT	TAATAACTTG	TGGATAACTG	GAAAGTTGAT	AACAATTTGG	3700
AGGACCAAAC	GACATGAAAA	TCACCATTTT	AGCTGTAGGG	AAACTAAAAAG	3750
AGAAATATTG	GAAGCAAGCC	ATAGCAGAAT	ATGAAAAACG	TTTAGGCCCA	3800
TACACCAAGA	TAGACATCAT	AGAAGTTCCA	GACGAAAAAG	CACCAGAAAA	3850
TATGAGCGAC	AAAGAAATTG	AGCAAGTAAA	AGAAAAAGAA	GGCCAACGAA	3900
TACTAGCCAA	AATTAAACCA	CAATCCACAG	TCATTACATT	AGAAATACAA	3950
GGAAAGATGC	TATCTTCCGA	AGGATTGGCC	CAAGAATTGA	ACCAACGCAT	4000
GACCCAAGGG	CAAAGCGACT	TTGTATTTCG	CATTGGCGGA	TCAAACGGCC	4050
TGCACAAGGA	CGTCTTACAA	CGCAGTAACT	ACGCACTATC	ATTTCAGCAA	4100
ATGACATTCC	CACATCAAAT	GATGCGGGTT	GTGTTAATTG	AGCAAGTGTA	4150
TAGAGCATTT	AAGATTATGC	GTGGAGAAGC	ATATCATAAA	TGA	4193

2) INFORMATION FOR SEQ ID NO: 232

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2996 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: 85/2082
- (C) ACCESSION NUMBER: Extracted from AB037671

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232

ATGAAACGAG	CCATTGGTTA	TTTGCGCCAA	AGTACAACGA	AACAACAATC	50
ACTCCCAGCT	CAAAAGCAAG	CAATAGAATT	ATTAGCTCCA	AAGCACAATA	100
TTCAAAATAT	CCAATACATT	AGTGATAAGC	AATCAGGCAG	AACAGATAAT	150
CGAACAGGCT	ATCAACAAGT	CACCGAACGC	ATCCAACAAA	GACAATGTGA	200
CGTATTATGT	TGTTATCGCT	TGAATCGACT	TCATCGCAAC	TTGAAAAATG	250
CATTAAAACT	CATGAAACTC	TGTCAAAAAT	ATCATGTTCA	TATTCTAAGT	300
GTTTCATGATG	GCTATTTTGA	TATGGATAAA	GCGTTTGATC	GCCTAAAACT	350
CAATATATTC	ATGAGTCTGG	CTGAACTTGA	ATCCGATAAT	ATTGGAGAAC	400
AAGTCAAAAA	TGGACTTAGA	GAAAAGGCAA	AACAAGGTAA	ACTCATAACG	450
ACCCATGCGC	CTTTCGGTTA	TCACTATCAA	AATGGTACTT	TCATCATTTAA	500
TAATGATGAA	TCACCTACCG	TCAAAGCTGT	ATTCAATTAT	TATCTTCAAG	550
GATATGGCTA	CAAGAAGATT	GCACAATATT	TAGAAGACGA	TAATAAACTT	600
ATTACCCGCA	AGCCTTATCA	GGTACGAAAT	ATAATTATGA	ACCCAAATTA	650
TTGTGGTCGT	GTCATCAATC	AATATGGTCA	ATATAACAAT	ATGGTACCAC	700
CTATTGTTTC	GGCAACGAAA	TATGAACATG	CTCAAGCAAT	CCGTAATAAG	750
AAGCAACTTC	ACTGTATACC	TTCAGAGAAT	CAGCTGAAAC	AAAAGATCAA	800
ATGTCCTTGT	TGTGACTCAA	CACTGACAAA	TATGACAATA	AGAAAAAAAC	850
ATACATTGCG	ATATTATATT	TGTCCTAAAA	ATATGAATGA	ATCTCGCTTT	900
GTCTGTTTCA	TCAAAGGAAT	AAATGCACAA	AAATTAGAAG	TTCAAGTCTT	950
AGCTACATGT	CAGAACTTCT	TTCAAAAACCA	ACAGCTCTAT	TCAAAAATTA	1000
ATAATGCAAT	TCATCAACGC	CTCAAAAAAC	AAAGAGTGAT	AGAAGCTAAA	1050
AGTACGCTAA	CTCAAGAACA	ACTGATAGAT	AAACTTGCCA	AAGGTATGAT	1100

TGATGCTGAA	TCATTTCAGAA	AACAGACTCA	TTTGATGAAT	CAAAAGCACA	1150
AAACCATATC	CTCCATAAGT	GATAATCAGT	TACAAACATC	ACTACAAAAG	1200
GTTATACAGA	AAAGTTTCAC	GTTAAACATG	CTGCATCCCT	ATATTGATGA	1250
AATTCGCATT	ACAAAAAATA	AAGCCCTTGT	TGGGATCTAT	TTCAAAAATG	1300
AACCATTGAA	CATTGTGAAC	CAAACCTCGC	AATCATCGAT	TGCTTAATCA	1350
GAAAGGATGA	AAAAATCATG	CAACAACCTCA	AACAAAAACG	TGTCGGTATC	1400
TATGTTTCGTG	TATCAACGGA	AATCCAAAGT	ACTGAAGGCT	ATAGTATCGA	1450
TGGACAAATC	AATCAAATTC	GAGAATATTG	TGATTTCAAT	AACCTTTGTTG	1500
TTGTAGATGT	ATACGCGGAT	AGAGGTATCT	CTGGAAAATC	TATGAACCGA	1550
CCAGAACTAC	AACGTTTGT	AAAAGATGCG	AACGAAGGTC	AGATTGATTTC	1600
TGTTATGGTC	TACAAAACAA	ACCGACTAGC	ACGTAACACT	TCTGACTTAC	1650
TCAAAATTGT	TGAAGACCTT	CATCGTCAAA	ATGTCGAATT	CTTCAGCTTA	1700
TCTGAGCGTA	TGGAAGTCAA	TACAAGCAGT	GGTAAATTGA	TGCTACAAAT	1750
TCTAGCGAGT	TTTTTCAGAAT	TTGAAAGAAA	TAATATTGTC	GAAAATGTAT	1800
TCTATGGTCA	AACCCGACGC	GCTCAAGAAG	GCTATTATCA	AGGCAATTTG	1850
CCGCTGGGCT	ATGACAAAAT	ACCGATATAG	AAGCATGAAC	TCATGATAAA	1900
CCAACATGAA	GCGAATATTG	TCAAATATAT	ATTTGAGTCA	TATGCTAAAG	1950
GCCACGGATA	TCGTAAAATT	TCCAATATAT	TCAATCACAA	AGGATACGTG	2000
ACTAAAAAAG	GAAAGCCTTT	CAGTATTGGT	TCAGTGACCT	ATATCTTATC	2050
TAATCCATTTC	TATGTTGGTA	AAATTCAATT	CGCAAAGTAC	AAAGATTGGA	2100
ATGAAAAGCG	TCGTAAAGGG	CTGAATGATA	AACCAATAAT	AGCTGAAGGT	2150
AAGCATTTCCC	CTATTATTAT	TCAAGACTTA	TGGGATAAAG	TCCAATTACG	2200
TAAAAAACAA	GTCAGTCAAA	AACCTCAAGT	CCACGGTAAA	GGAACATAATC	2250
TATTAACAGG	TATCGTTCAT	TGTCCACAAT	GTGGTGCACC	AATGGCAGCT	2300
AGTAACACAA	CGAACACATT	GAAAGATGGT	ACCAAGAAGC	GAATACGTTA	2350
TTATTCTTGC	AGTAACTTCC	GAAACAAAGG	CTCAAAAGTA	TGTTCTGCGA	2400
ATAGCGTTAG	AGCTGATGTG	ATTGAGAAAT	ACGTCATGGA	TCAAATACTC	2450
GAAATTGTCA	AAAGTGATAA	AGTCATTAAC	CAAGTCTTAG	AACGTGTCAA	2500
TCAAGAAAAT	AAAGTCGATA	TTGGTGCATT	GAACCACGAT	ATCGCTTATA	2550
AACAACAACA	ATACGATGAA	GTCAGCGGGA	AACCTCCATAA	TTTAGTTAAA	2600
ACCATTGAAG	ATAATCCGGA	CCTAACATCT	GCATTGAAAG	CAACTATTCA	2650
TCAATATGAA	ACACAACCTCA	ATGACATTAC	AAATCAAATG	AATCAACTCA	2700
AACAGCAACA	AAATCAAGAG	AAACTATCTT	ATGATACGAA	ACAAATCGCT	2750
GCCCTATTAC	AACGAATATT	TCAAAATATA	GAATCAATGG	ATAAAGCACA	2800
ACTCAAAGCA	TTATATCTTA	CAGTCATTGA	CCGTATTGAT	ATTTCGTAAAG	2850
ACGGTAATCA	TAAAAAACAG	TTCTACGTTA	CACATAAACT	CAATAATGAA	2900
ATTATTAAAC	AACTTTTCAA	TAATACCCCT	CTCGACGAAG	TGCTCCTCAG	2950
CACTTCGTCT	TTATTTTTTGC	CTCAAACGCT	CTTTCTTCAA	ATCTAA	2996

2) INFORMATION FOR SEQ ID NO: 233

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1410 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: CCRI-9681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233

GCTGTAGGGA	AACTAAAAGA	GAAATATTGG	AAGCAAGCCA	TAGCAGAATA	50
TGAAAAACGT	TTAGGCCCAT	ACACCAAGAT	AGACATCATA	GAAGTTCCAG	100
ACGAAAAAGC	ACCAGAAAAT	ATGAGCGACA	AAGAAATTGA	GCAAGTAAAA	150
GAAAAAGAAG	GCCAACGAAT	ACTAGCCAAA	ATTAAACCAC	AATCCACAGT	200
CATTACATTA	GAAATACAAG	GAAAGATGCT	ATCTTCCGAA	GGATTGGCCC	250
AAGAATTGAA	CCAACGCATG	ACCCAAGGGC	AAAGCGACTT	TGTATTTCGTC	300
ATTGGCGGAT	CAAACGGCCT	GCACAAGGAC	GTCTTACAAC	GCAGTAACTA	350
CGCACTATCA	TTCAGCAAAA	TGACATTCCC	ACATCAAATG	ATGCGGGTTG	400
TGTTAATTGA	GCAAGTGTAT	AGAGCATTTA	AGATTATGCG	TGGAGAAGCA	450
TATCATAAAT	GATGCGGTTT	TTTCAGCCGC	TTCATAAAGG	GATTTTGAAT	500
GTATCAGAAC	ATATGAGGTT	TATGTGAATT	GCTGTTATGT	TTTTAAGAAG	550
CATATCATAA	GTGATGCGGT	TTTTATTAAAT	TAGTTGCTAA	AAAATGAAGT	600
ATGCAATATT	AATTATTATT	AAATTTTGAT	ATATTTAAAG	AAAGATTAAAG	650
TTTAGGGTGA	ATGAATGGCT	TATCAAAGTG	AATATGCATT	AGAAAATGAA	700
GTA CTTCAAC	AACTTGAGGA	ATTGAACTAT	GAAAGAGTAA	ATATACATAA	750
TATTAAATTA	GAAATTAATG	AATATCTCAA	AGA A CTAGGA	GTGTTGAAAA	800
ATGAATAAGC	AGACAAATAC	TCCAGAACTA	AGATTTCCAG	AGTTTGATGA	850
GGAATGGAAA	AAAAGGAAAT	TAGGTGAAGT	AGTAAATTAT	AAAAATGGTG	900
GTTCAATTGA	AAGTTTAGTG	AAAAACCATG	GTGTATATAA	ACTCATAACT	950
CTTAAATCTG	TTAATACAGA	AGGAAAGTTG	TGTAATTCTG	GAAAAATATAT	1000
CGATGATAAA	TGTGTTGAAA	CATTGTGTAA	TGATACTTTA	GTAATGATAC	1050
TGAGCGAGCA	AGCACCAGGA	CTAGTTGGAA	TGACTGCAAT	TATACCTAAT	1100
AATAATGAGT	ATGTACTAAA	TCAACGAGTA	GCAGCACTAG	TGCCTAAACA	1150
ATTTATAGAT	AGTCAATTTC	TATCTAAGTT	AATTAATAGA	AACCAGAAAT	1200
ATTTCACTGT	GAGATCTGCT	GGAACAAAAG	TGAAAAATAT	TTCTAAAGGA	1250
CATGTAGAAA	ACTTTAATTT	TTTATCTCCT	AATTACACTG	AACAACAAAA	1300
AATAGGTAAT	TTCTTCAGCA	AACTCGACCG	CCAGATTGAG	TTAGAAGAAG	1350
AGAAACTTGA	ACTCTTATAG	CAACAAAAGC	GTGGATATAT	TTCAGAAGAT	1400
TTTTCTCAAG					1410

INTERNATIONAL SEARCH REPORT

International Application No.

PCT/CA 02/00824

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

BIOSIS, EPO-Internal, MEDLINE, EMBL, EMBASE, PAJ, WPI Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	ITO T ET AL: "Structural comparison of three types of staphylococcal cassette chromosome mec integrated in the chromosome in methicillin-resistant <i>Staphylococcus aureus</i> ." ANTIMICROBIAL AGENTS AND CHEMOTHERAPY. UNITED STATES MAY 2001, 'Online! vol. 45, no. 5, May 2001 (2001-05), pages 1323-1336, XP002238384 ISSN: 0066-4804 cited in the application page 1334, left-hand column, paragraph 3 -right-hand column, paragraph 2; figures 1,2; tables 1,2 page 1335, left-hand column, paragraph 2 page 1335, right-hand column, paragraph 2 -& DATABASE EMBL 'Online! 14 May 2001 (2001-05-14) retrieved from EBI	1-20
X	-/--	14, 17, 18

☒ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

* Special categories of cited documents:

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
- *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

T later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

X document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

Y document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

Z document member of the same patent family

Date of the actual completion of the international search

15 April 2003

Date of mailing of the international search report

24. 09. 03

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2
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Rutz, B

INTERNATIONAL SEARCH REPORT

International Application No.

PCT/CA 02/00824

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
	Database accession no. AB037671 XP002238391 abstract ----	
X	DATABASE EMBL 'Online! 7 January 2000 (2000-01-07) retrieved from EBI Database accession no. AB014433 XP002238392 abstract ----	14,17,18
Y	EP 0 887 424 A (KAINOS LAB INC) 30 December 1998 (1998-12-30) page 3, line 2 - line 10 page 4, line 28 - line 35 page 6, line 30 - line 34; figures 1-3,5,8 ----	1-20
A	HIRAMATSU K ET AL: "Genetic Basis fo Molecular Epidemiology of MRSA" J INFECT CHEMOTHER, vol. 2, 1996, pages 117-129, XP001122060 cited in the application page 120, left-hand column, paragraph 2 -right-hand column, paragraph 1; figures 2,4 page 122, left-hand column, paragraph 1 page 123, right-hand column, paragraph 1 -page 124, left-hand column, paragraph 1 ----	
A	OLIVEIRA D C ET AL: "Genetic organization of the downstream region of the mecA element in methicillin-resistant Staphylococcus aureus isolates carrying different polymorphisms of this region." ANTIMICROBIAL AGENTS AND CHEMOTHERAPY. UNITED STATES JUL 2000, vol. 44, no. 7, July 2000 (2000-07), pages 1906-1910, XP002238385 ISSN: 0066-4804 page 1906, left-hand column, paragraphs 1,2; figures 1,2; tables 2,3 page 1908, right-hand column, paragraphs 1,2 page 1909, left-hand column, paragraph 3 -right-hand column, paragraph 3 ----	
A	ITO T ET AL: "Cloning and nucleotide sequence determination of the entire mec DNA of pre-methicillin-resistant Staphylococcus aureus N315." ANTIMICROBIAL AGENTS AND CHEMOTHERAPY. UNITED STATES JUN 1999, vol. 43, no. 6, June 1999 (1999-06), pages 1449-1458, XP002238386 ISSN: 0066-4804 ----	

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INTERNATIONAL SEARCH REPORT

International Application No

PCT/CA 02/00824

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>KATAYAMA Y ET AL: "A new class of genetic element, staphylococcus cassette chromosome mec, encodes methicillin resistance in Staphylococcus aureus." ANTIMICROBIAL AGENTS AND CHEMOTHERAPY. UNITED STATES JUN 2000, vol. 44, no. 6, June 2000 (2000-06), pages 1549-1555, XP002238387 ISSN: 0066-4804</p>	
A	<p>KURODA M ET AL: "Whole genome sequencing of methicillin-resistant Staphylococcus aureus" LANCET THE, LANCET LIMITED. LONDON, GB, vol. 357, no. 9264, 21 April 2001 (2001-04-21), pages 1225-1240, XP004246103 ISSN: 0140-6736 page 1234, right-hand column, paragraph 3 page 1238, left-hand column, paragraph 3; figure 1</p>	
P,X	<p>MA XIAO XUE ET AL: "Novel type of staphylococcal cassette chromosome mec identified in community-acquired methicillin-resistant Staphylococcus aureus strains." ANTIMICROBIAL AGENTS AND CHEMOTHERAPY, vol. 46, no. 4, April 2002 (2002-04), pages 1147-1152, XP002238388 April, 2002 ISSN: 0066-4804 cited in the application figures 1,2 & DATABASE EMBL 'Online! 21 November 2001 (2001-11-21) retrieved from EBI Database accession no. AB063172 abstract & DATABASE EMBL 'Online! 21 November 2001 (2001-11-21) retrieved from EBI Database accession no. AB063173 abstract</p>	1-20

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INTERNATIONAL SEARCH REPORT

International Application No

PCT/CA 02/00824

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	<p>OLIVEIRA D C ET AL: "The evolution of pandemic clones of methicillin-resistant Staphylococcus aureus: identification of two ancestral genetic backgrounds and the associated mec elements." MICROBIAL DRUG RESISTANCE (LARCHMONT, N.Y.) UNITED STATES 2001 WINTER, vol. 7, no. 4, January 2001 (2001-01), pages 349-361, XP009004903 ISSN: 1076-6294 cited in the application page 352, left-hand column, paragraph 4 -right-hand column, paragraph 5; figure 1; tables 2,3 page 355, left-hand column, paragraph 6 -right-hand column, paragraph 4 & DATABASE EMBL 'Online! 8 March 2002 (2002-03-08) retrieved from EBI Database accession no. AF411934 abstract & DATABASE GENBANK 'Online! 5 March 2002 (2002-03-05) retrieved from NCBI Database accession no. AF411935 abstract & DATABASE GENBANK 'Online! 5 March 2002 (2002-03-05) retrieved from NCBI Database accession no. AF411936 abstract</p>	1-20
P,X	<p>--- BABA TADASHI ET AL: "Genome and virulence determinants of high virulence community-acquired MRSA." LANCET. ENGLAND 25 MAY 2002, vol. 359, no. 9320, 25 May 2002 (2002-05-25), pages 1819-1827, XP002238389 ISSN: 0140-6736 page 1823, left-hand column, paragraph 2 -right-hand column, paragraph 1; figures 2-4; tables 1,2 & DATABASE EMBL 'Online! 27 May 2002 (2002-05-27) retrieved from EBI Database accession no. AP004822 abstract</p> <p>---</p>	1-20

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INTERNATIONAL SEARCH REPORT

International Application No.

PCT/CA 02/00824

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,A	<p>HIRAMATSU KEIICHI ET AL: "The emergence and evolution of methicillin-resistant Staphylococcus aureus." TRENDS IN MICROBIOLOGY, vol. 9, no. 10, October 2001 (2001-10), pages 486-493, XP002238390 page 492, right-hand column, paragraph 2; figures 1-5; table 1 -----</p>	

INTERNATIONAL SEARCH REPORT

International application No.
PCT/CA 02/00824

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-20 (all partially)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1: claims 1-20 (all partially)

nucleic acids derived from *Staphylococcus aureus* MREJ type iv, oligonucleotides hybridizing with said nucleic acids, oligonucleotide pairs for the detection of MREJ type iv, method to detect the presence of methicillin-resistant *Staphylococcus aureus* of MREJ type iv

Invention 2: claims 1-20 (all partially)

nucleic acids derived from *Staphylococcus aureus* MREJ type v, oligonucleotides hybridizing with said nucleic acids, oligonucleotide pairs for the detection of MREJ type v, method to detect the presence of methicillin-resistant *Staphylococcus aureus* of MREJ type v

Invention 3: claims 1-20 (all partially)

nucleic acids derived from *Staphylococcus aureus* MREJ type vi, oligonucleotides hybridizing with said nucleic acids, oligonucleotide pairs for the detection of MREJ type vi, method to detect the presence of methicillin-resistant *Staphylococcus aureus* of MREJ type vi

Invention 4: claims 1-20 (all partially)

nucleic acids derived from *Staphylococcus aureus* MREJ type vii, oligonucleotides hybridizing with said nucleic acids, oligonucleotide pairs for the detection of MREJ type vii, method to detect the presence of methicillin-resistant *Staphylococcus aureus* of MREJ type vii

Invention 5: claims 1-20 (all partially)

nucleic acids derived from *Staphylococcus aureus* MREJ type viii, oligonucleotides hybridizing with said nucleic acids, oligonucleotide pairs for the detection of MREJ type viii, method to detect the presence of methicillin-resistant *Staphylococcus aureus* of MREJ type viii

Invention 6: claims 1-20 (all partially)

nucleic acids derived from *Staphylococcus aureus* MREJ type ix, oligonucleotides hybridizing with said nucleic acids, oligonucleotide pairs for the detection of MREJ type ix, method to detect the presence of methicillin-resistant *Staphylococcus aureus* of MREJ type ix

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Invention 7: claim 1 (partially)

method to detect the presence of methicillin-resistant
Staphylococcus aureus of MREJ type x

Invention 8: claim 15 (partially)

oligonucleotide pairs for the detection of MREJ type i

Invention 9: claim 15 (partially)

oligonucleotide pairs for the detection of MREJ type ii

Invention 10: claim 15 (partially)

oligonucleotide pairs for the detection of MREJ type iii

Information on patent family members

PCT/CA 02/00824

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
EP 0887424 A	30-12-1998	JP 9224700 A	02-09-1997
		AU 696462 B2	10-09-1998
		AU 1810997 A	10-09-1997
		CA 2218476 A1	28-08-1997
		EP 0887424 A2	30-12-1998
		US 6156507 A	05-12-2000
		WO 9731125 A2	28-08-1997